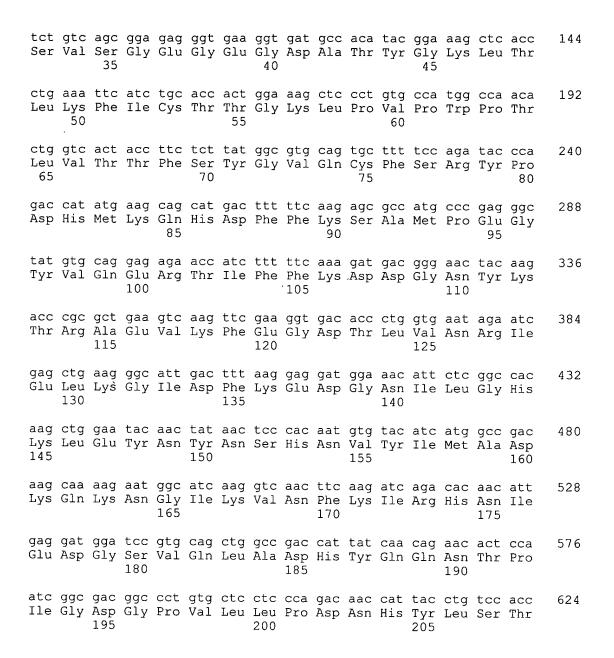
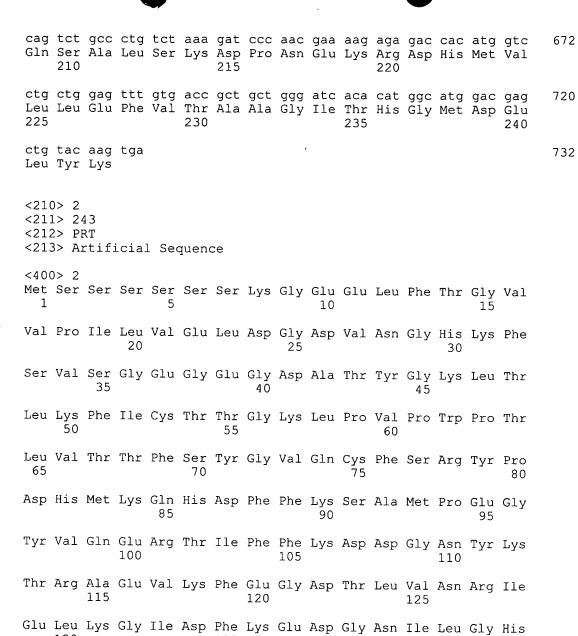
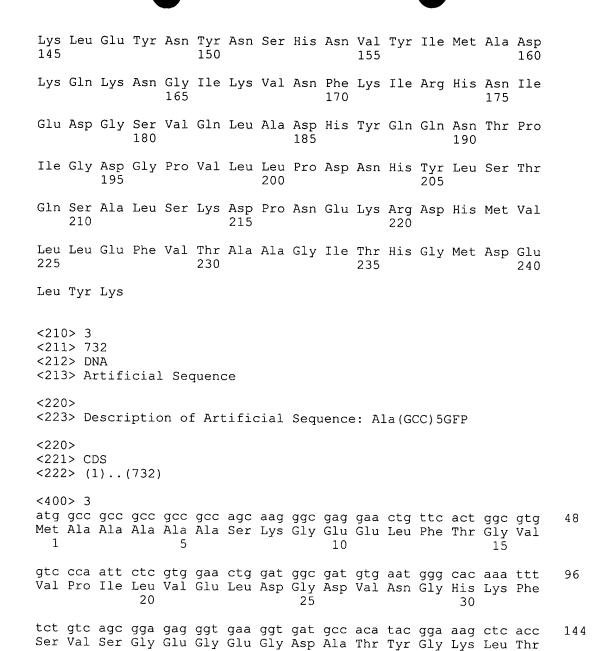
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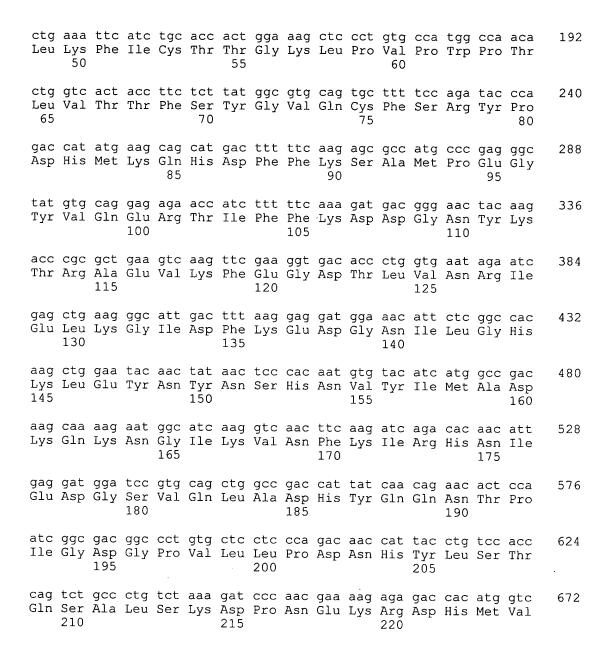
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- <130> 10338-5US
- <140> Not yet assigned
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- <150> AU PP8078
- <151> 1999-01-08
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- <223> Description of Artificial Sequence: Ala(GCA)5GFP
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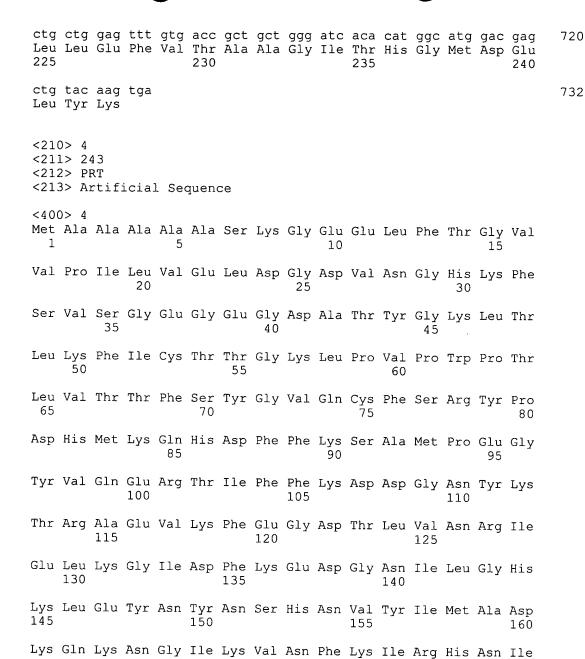




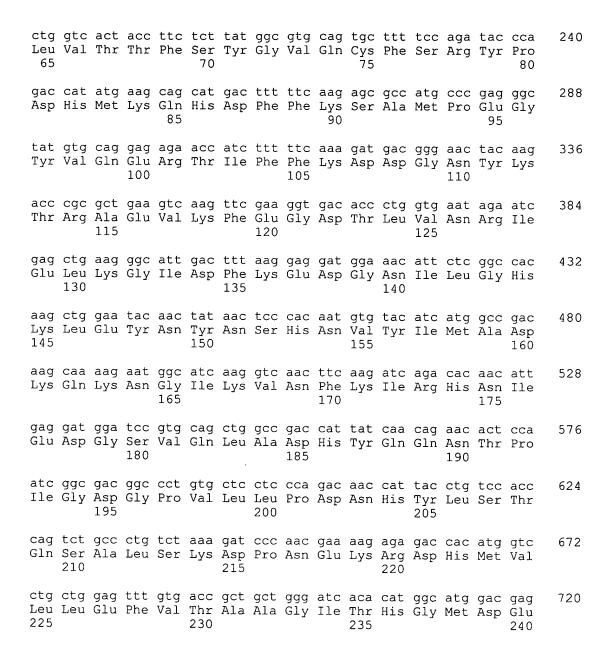


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Ile	Gly	Asp 195	Gly	Pro	Val	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr	
Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val	
Leu 225	Leu	Glu	Phe	Val	Thr 230	Ala	Ala	Gly	Ile	Thr 235	His	Gly	Met	Asp	Glu 240	
Leu	Tyr	Lys														
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gtc Val	cca Pro	att Ile	ctc Leu 20	gtg Val	gaa Glu	ctg Leu	gat Asp	ggc Gly 25	gat Asp	gtg Val	aat Asn	ggg Gly	cac His 30	aaa Lys	ttt Phe	96
tct Ser	gtc Val	agc Ser 35	gga Gly	gag Glu	ggt Gly	gaa Glu	ggt Gly 40	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly 45	aag Lys	ctc Leu	acc Thr	144
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<211> 243

<212> PRT

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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

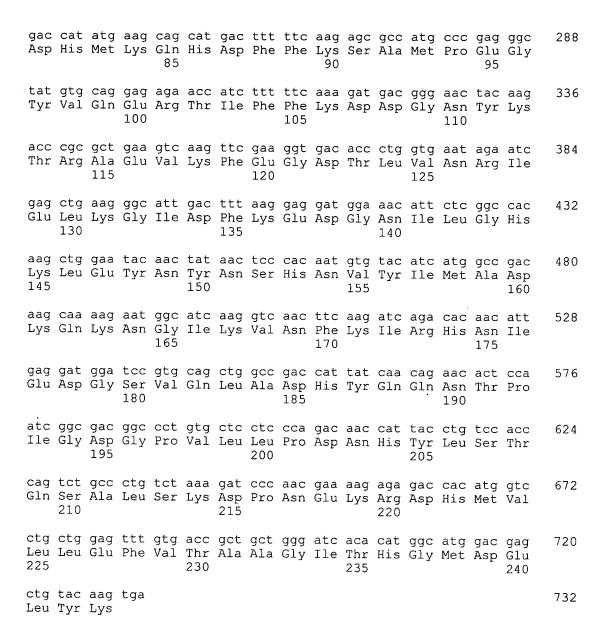
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Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile	Gly	Asp 195	Gly	Pro	Val	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr	
Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val	
Leu 225	Leu	Glu	Phe	Val	Thr 230	Ala	Ala	Gly	Ile	Thr 235	His	Gly	Met	Asp	Glu 240	
Leu	Tyr	Lys														
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gtc Val	cca Pro	att Ile	ctc Leu 20	gtg Val	gaa Glu	ctg Leu	gat Asp	ggc Gly 25	gat Asp	gtg Val	aat Asn	ggg Gly	cac His 30	aaa Lys	ttt Phe	96
tct Ser	gtc Val	agc Ser 35	gga Gly	gag Glu	ggt Gly	gaa Glu	ggt Gly 40	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly 45	aag Lys	ctc Leu	acc Thr	144
ctg Leu	aaa Lys 50	ttc Phe	atc Ile	tgc Cys	acc Thr	act Thr 55	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val 60	cca Pro	tgg Trp	cca Pro	aca Thr	192
ctg Leu 65	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser 70	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys 75	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro 80	240



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<211> 243

<212> PRT

<213> Artificial Sequence

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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

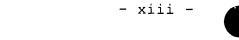
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205



Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 235

Leu Tyr Lys

<210> 9

<211> 732

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Arg(AGA)5GFP

<220>

<221> CDS

<222> (1)..(732)

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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 25

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 40

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 55

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 70

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90

tat Tyr	gtg Val	cag Gln	gag Glu 100	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	ggg Gly	aac Asn 110	tac Tyr	aag Lys	336
acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggt Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528
gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc Ile	ggc Gly	gac Asp 195	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	Gly aaa	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
	tac Tyr		tga													732

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<213> Artificial Sequence

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Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

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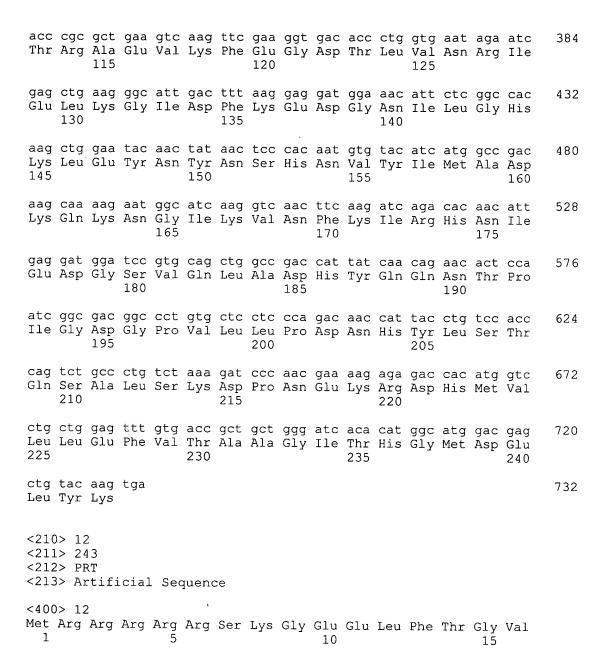
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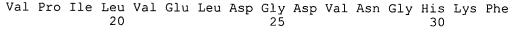
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Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu

225 230 235 240 Leu Tyr Lys <210> 11 <211> 732 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Arg(AGG)5GFP <220> <221> CDS <222> (1) ... (732) <400> 11 atg agg agg agg agg agc aag ggc gag gaa ctg ttc act ggc gtg 48 Met Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val 10 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys





Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

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Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

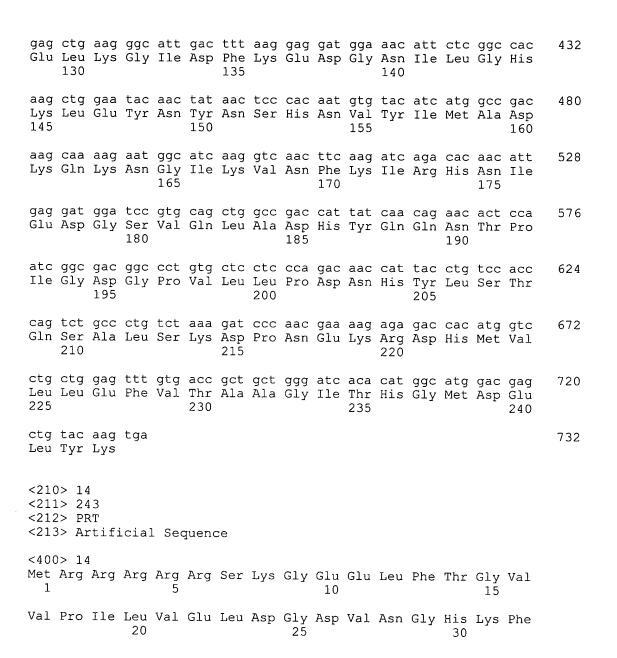
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Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

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Leu Tyr Lys

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gtc Val	cca Pro	att Ile	ctc Leu 20	gtg Val	gaa Glu	ctg Leu	gat Asp	ggc Gly 25	gat Asp	gtg Val	aat Asn	Gly	cac His 30	aaa Lys	ttt Phe	96
tct Ser	gtc Val	agc Ser 35	gga Gly	gag Glu	ggt Gly	gaa Glu	ggt Gly 40	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly 45	aag Lys	ctc Leu	acc Thr	144
ctg Leu	aaa Lys 50	ttc Phe	atc Ile	tgc Cys	acc Thr	act Thr 55	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val 60	cca Pro	tgg Trp	cca Pro	aca Thr	192
ctg Leu 65	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser 70	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys 75	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro 80	240
gac Asp	cat His	atg Met	aag Lys	cag Gln 85	cat His	gac Asp	ttt Phe	ttc Phe	aag Lys 90	agc Ser	gcc Ala	atg Met	ccc Pro	gag Glu 95	ggc Gly	288
tat Tyr	gtg Val	cag Gln	gag Glu 100	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	gly ggg	aac Asn 110	tac Tyr	aag Lys	336
acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggt Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384



Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

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Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

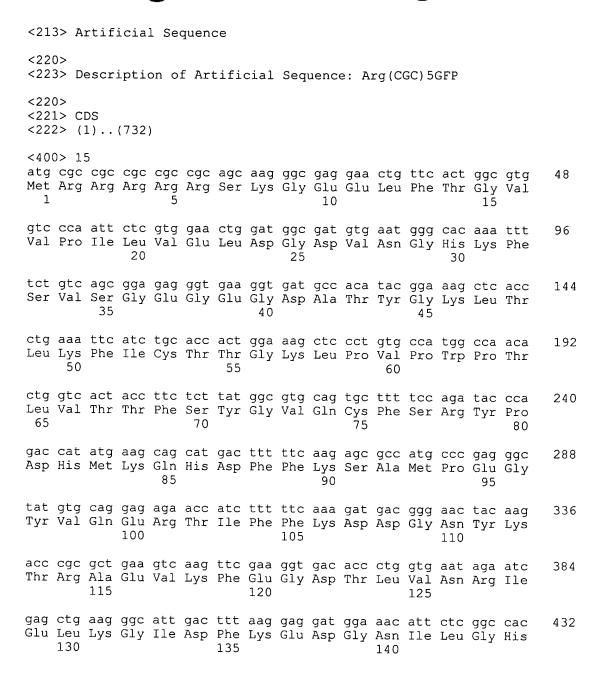
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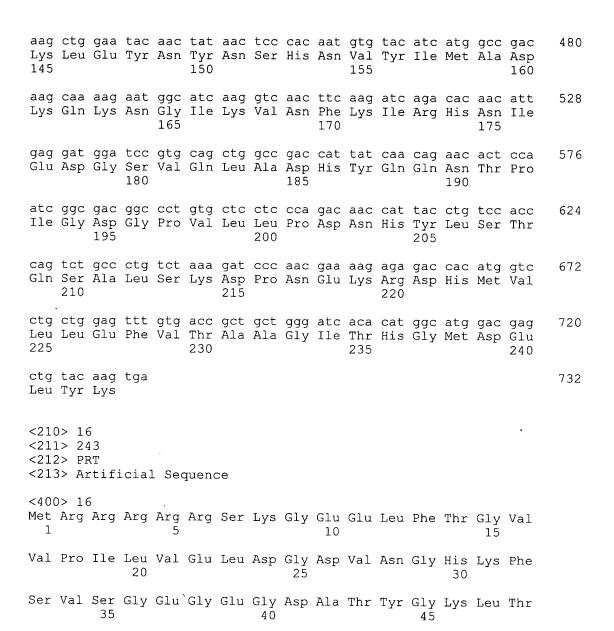
Leu Tyr Lys

<210> 15

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<212> DNA





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Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gl
n Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly As
n Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

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gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc Ile	ggc Gly	gac Asp 195	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	ggg Gly	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
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Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr	
Leu	Lys 50	Phe	Ile	Cys	Thr	Thr 55	Gly	Lys	Leu	Pro	Val 60	Pro	Trp	Pro	Thr	
Leu 65	Val	Thr	Thr	Phe	Ser 70	Tyr	Gly	Val	Gln	Cys 75	Phe	Ser	Arg	Tyr	Pro 80	

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro $180 \,$ $185 \,$ 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 .205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 235 240

Leu Tyr Lys

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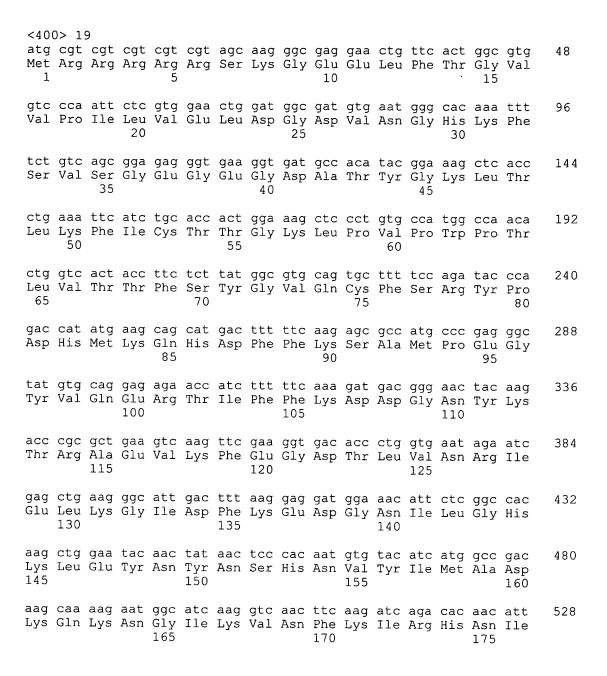
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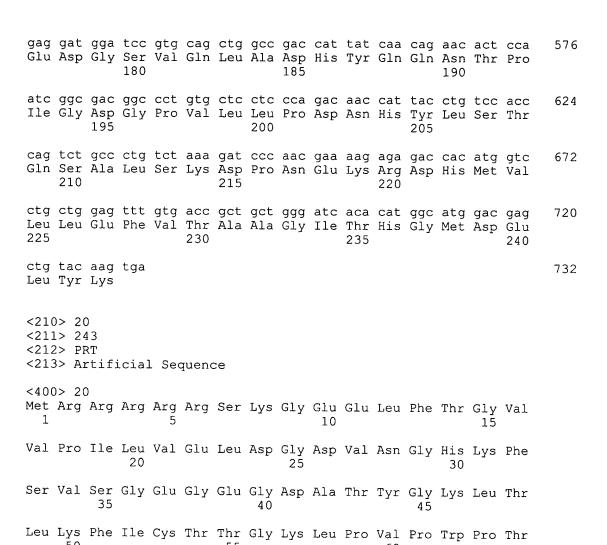
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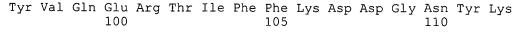
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Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly



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Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240

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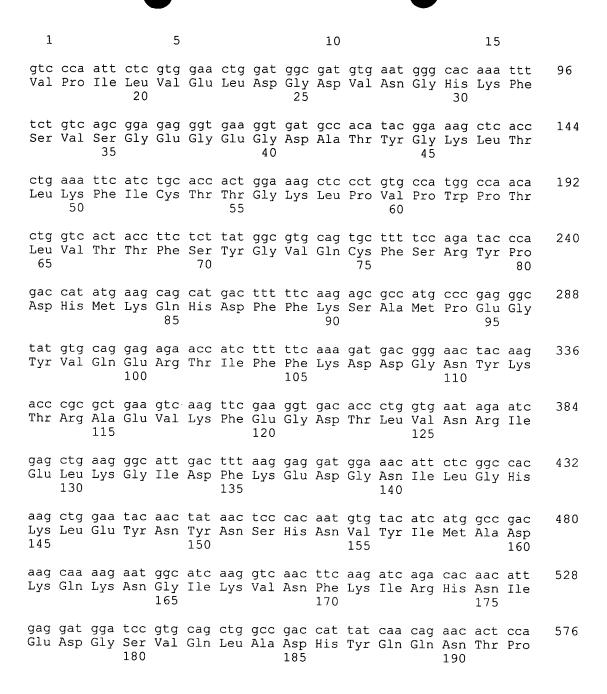
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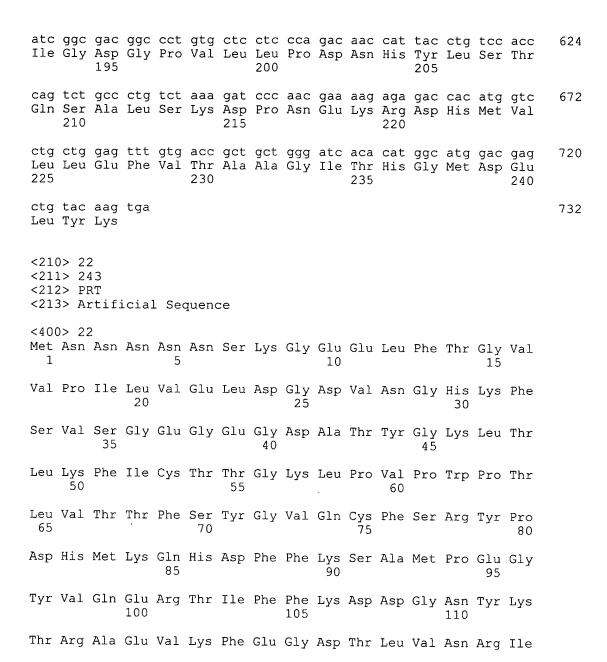
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- xxxiii -

115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 135

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 150 155

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 170

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 185

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 200

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<213> Artificial Sequence

<223> Description of Artificial Sequence: Asn(AAT)5GFP

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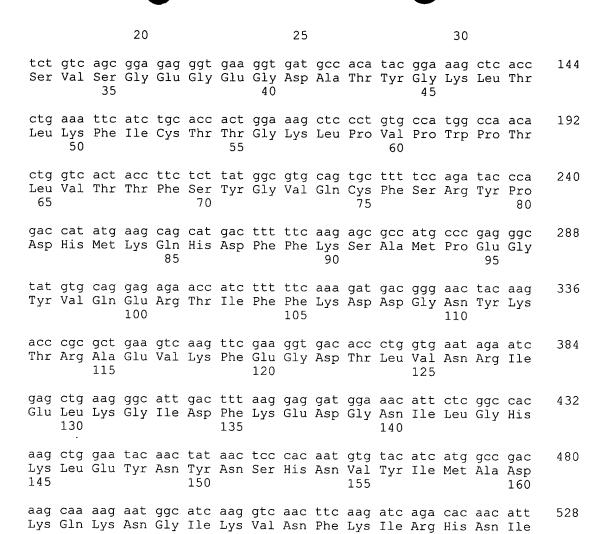
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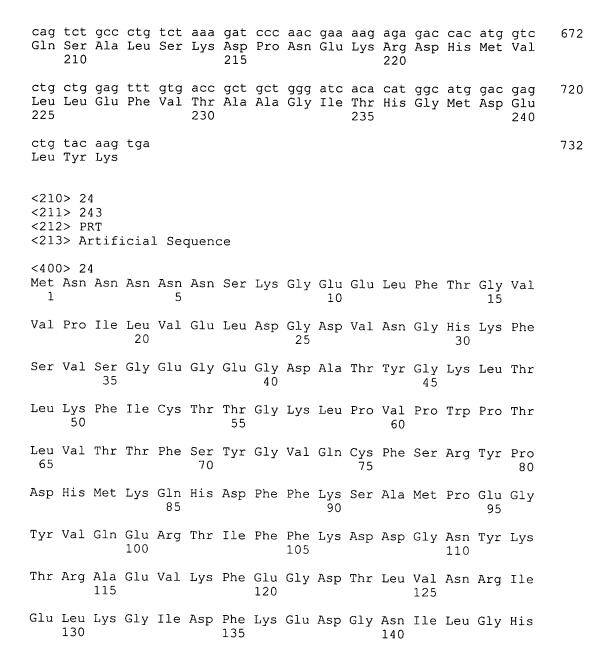


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Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr

624



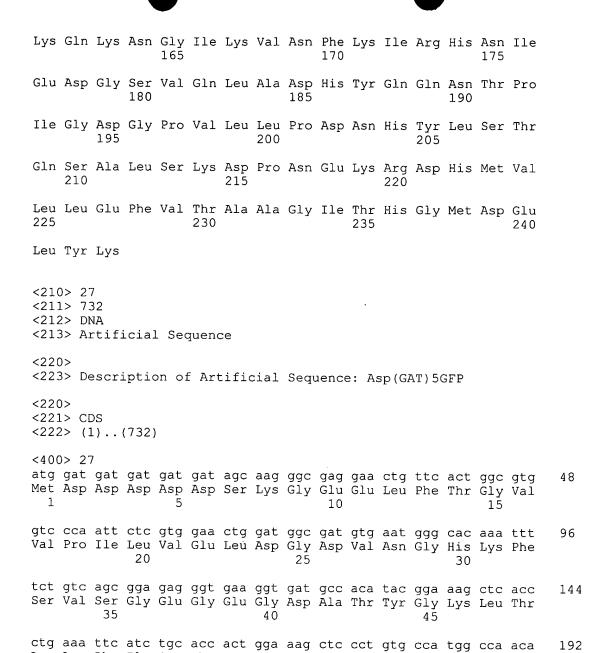
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Glu	Asp	Gly	Ser 180	Val	Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro	
Ile	Gly	Asp 195	Gly	Pro	Val	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr	
Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val	
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)> L> C[2> (1		(732)													
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gtc Val	cca Pro	att Ile	ctc Leu 20	gtg Val	gaa Glu	ctg Leu	gat Asp	ggc Gly 25	gat Asp	gtg Val	aat Asn	ggg Gly	cac His 30	aaa Lys	ttt Phe	96
tct Ser	gtc Val	agc Ser	gga Gly	gag Glu	ggt Gly	gaa Glu	ggt Gly	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly	aag Lys	ctc Leu	acc Thr	14





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ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	Gly	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
	tac Tyr	aag Lys	tga													732
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Val	Pro	Ile	Leu 20	Val	Glu	Leu	Asp	Gly 25	Asp	Val	Asn	Gly	His 30	Lys	Phe	
Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr	
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Tyr	Val	Gln	Glu 100	Arg	Thr	Ile	Phe	Phe 105	Lys	Asp	Asp	Gly	Asn 110	Tyr	Lys	
Thr	Arg	Ala 115	Glu	Val	Lys	Phe	Glu 120	Gly	Asp	Thr	Leu	Val 125	Asn	Arg	Ile	
Glu	Leu 130	Lys	Gly	Ile	Asp	Phe 135	Lys	Glu	Asp	Gly	Asn 140	Ile	Leu	Gly	His	
Lys 145	Leu	Glu	Tyr	Asn	Tyr 150	Asn	Ser	His,	Asn	Val 155	Tyr	Ile	Met	Ala	Asp 160	



Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr

50 55 60 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 70 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 135 aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 150 aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 170 gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 185 atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 200 cag tot goo otg tot aaa gat ooc aac gaa aag aga gac cac atg gto 672 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 215 ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 230 235

ctg tac aag tga Leu Tyr Lys 732

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<213> Artificial Sequence

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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
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Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

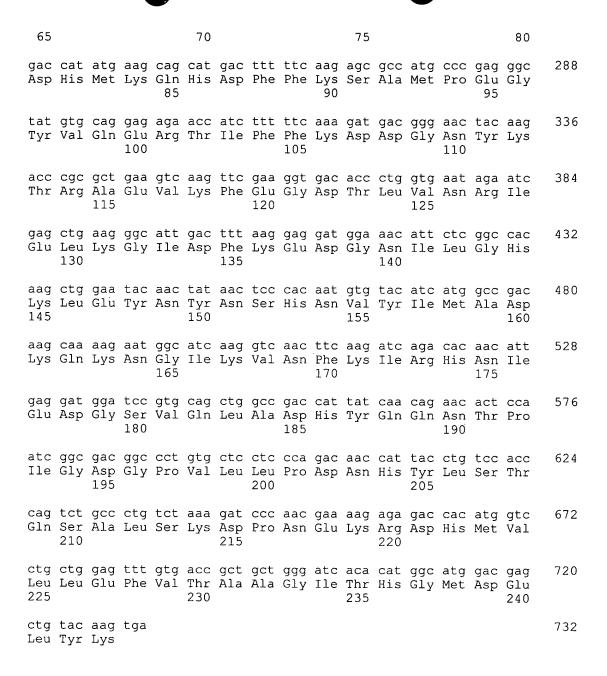
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Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro

180 185 190 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 Leu Tyr Lys <210> 29 <211> 732 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: Cys(TGC)5GFP <220> <221> CDS <222> (1)..(732) <400> 29 atg tgc tgc tgc tgc agc aag ggc gag gaa ctg ttc act ggc gtg Met Cys Cys Cys Cys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val 10 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 tet gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro



<210> 30

<211> 243

<212> PRT

<213> Artificial Sequence

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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

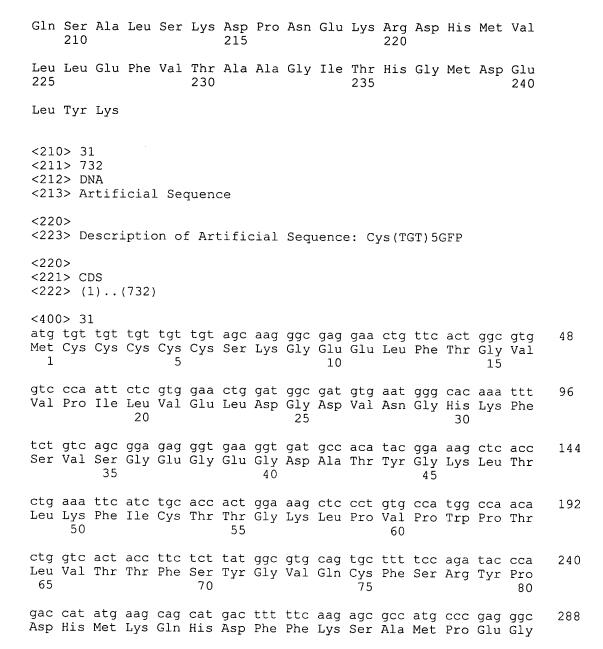
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

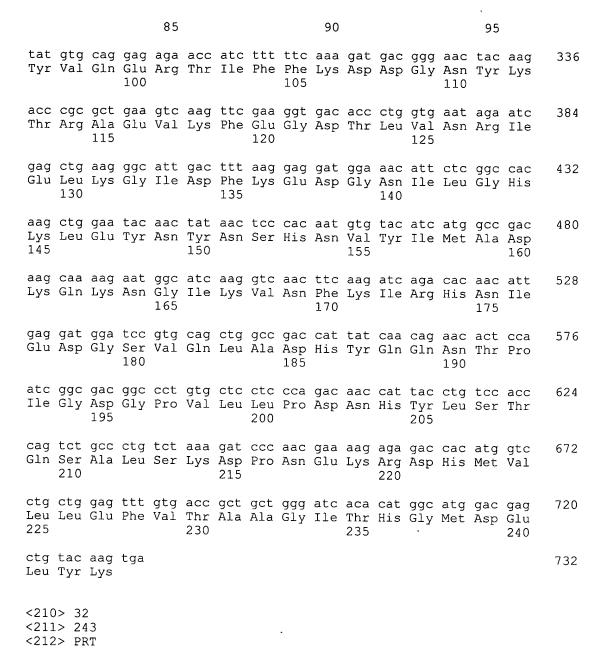
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Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205







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Met Cys Cys Cys Cys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val 1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

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Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220



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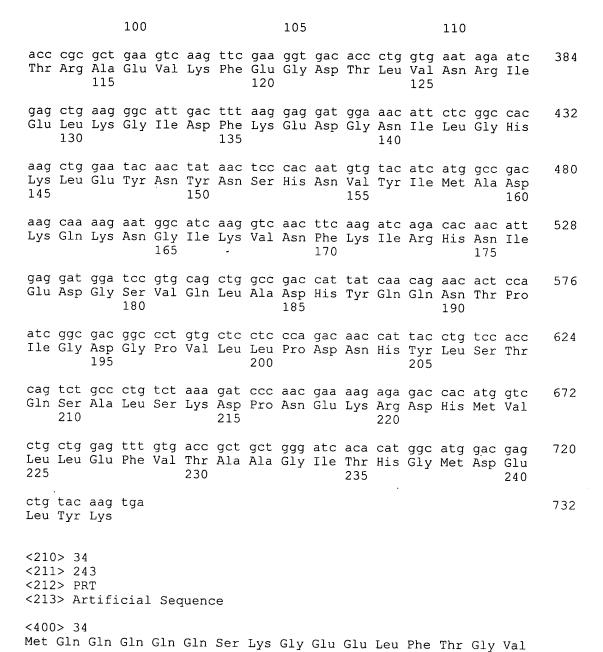
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ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys



-xlix-

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Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr
Leu	Lys 50	Phe	Ile	Cys	Thr	Thr 55	Gly	Lys	Leu	Pro	Val 60	Pro	Trp	Pro	Thr
Leu 65	Val	Thr	Thr	Phe	Ser 70	Tyr	Gly	Val	Gln	Cys 75	Phe	Ser	Arg	Tyr	Pro 80
Asp	His	Met	Lys	Gln 85	His	Asp	Phe	Phe	Lys 90	Ser	Ala	Met	Pro	Glu 95	Gly
Tyr	Val	Gln	Glu 100	Arg	Thr	Ile	Phe	Phe 105	Lys	Asp	Asp	Gly	Asn 110	Tyr	Lys
Thr	Arg	Ala 115	Glu	Val	Lys	Phe	Glu 120	Gly	Asp	Thr	Leu	Val 125	Asn	Arg	Ile
Glu	Leu 130	Lys	Gly	Ile	Asp	Phe 135	Lys	Glu	Asp	Gly	Asn 140	Ile	Leu	Gly	His
Lys 145	Leu	Glu	Tyr	Asn	Tyr 150	Asn	Ser	His	Asn	Val 155	Tyr	Ile	Met	Ala	Asp 160
Lys	Gln	Lys	Asn	Gly 165	Ile	Lys	Val	Asn	Phe 170	Lys	Ile	Arg	His	Asn 175	Ile
Glu	Asp	Gly	Ser 180	Val	Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro
Ile	Gly	Asp 195	Gly	Pro	Val	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr
Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val
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ctg Leu 65	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser 70	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys 75	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro 80	240
gac Asp	cat His	atg Met	aag Lys	cag Gln 85	cat His	gac Asp	ttt Phe	ttc Phe	aag Lys 90	agc Ser	gcc Ala	atg Met	ccc Pro	gag Glu 95	ggc Gly	288
tat Tyr	gtg Val	cag Gln	gag Glu 100	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	ggg Gly	aac Asn 110	tac Tyr	aag Lys	336
acc Thr	cgc Arg	gct Ala	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu	ggt Glv	gac Asp	acc Thr	ctg Leu	gtg Val	aat Asn	aga Arg	atc	384

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aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
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Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

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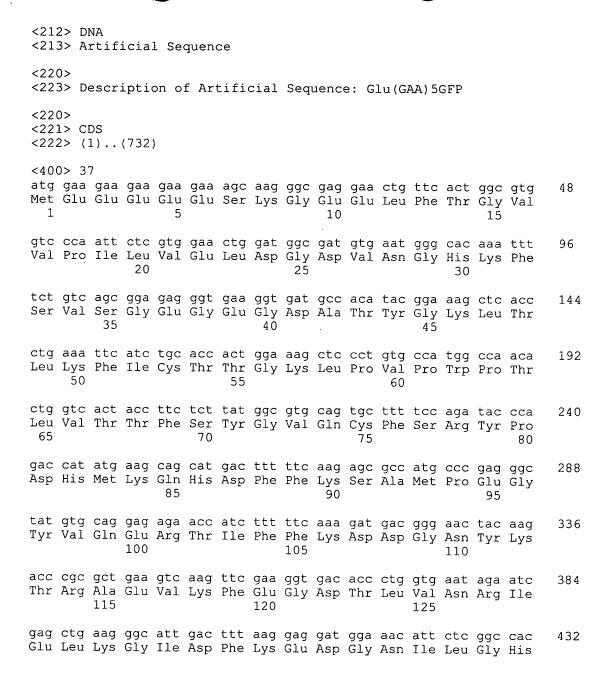
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Leu Tyr Lys

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Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

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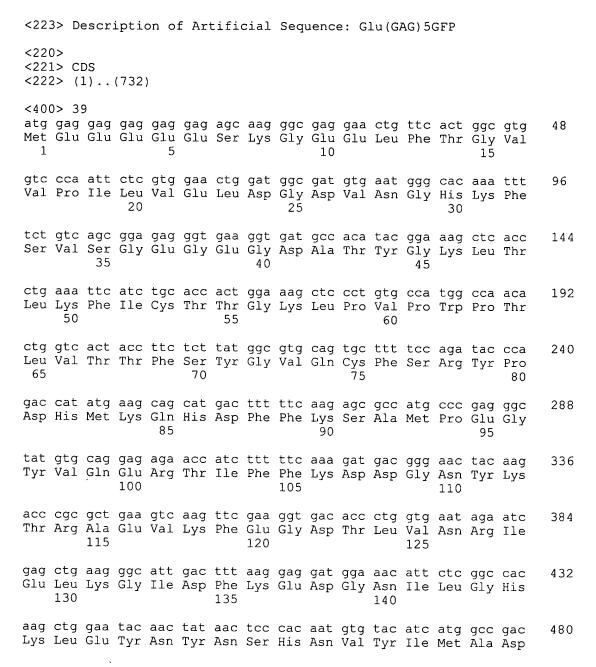
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528

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ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	ggg Gly	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
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Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

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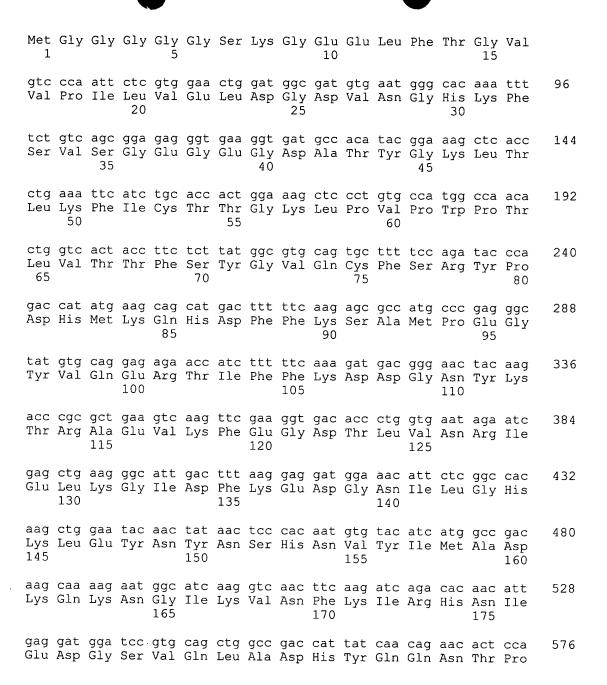
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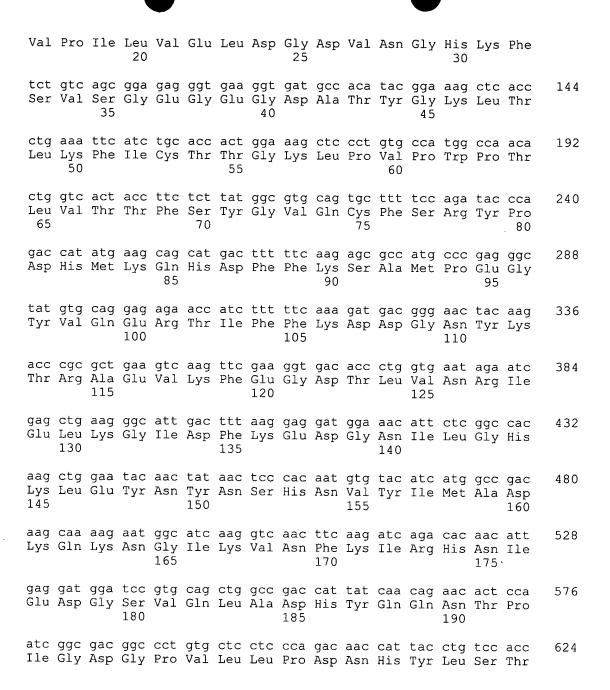
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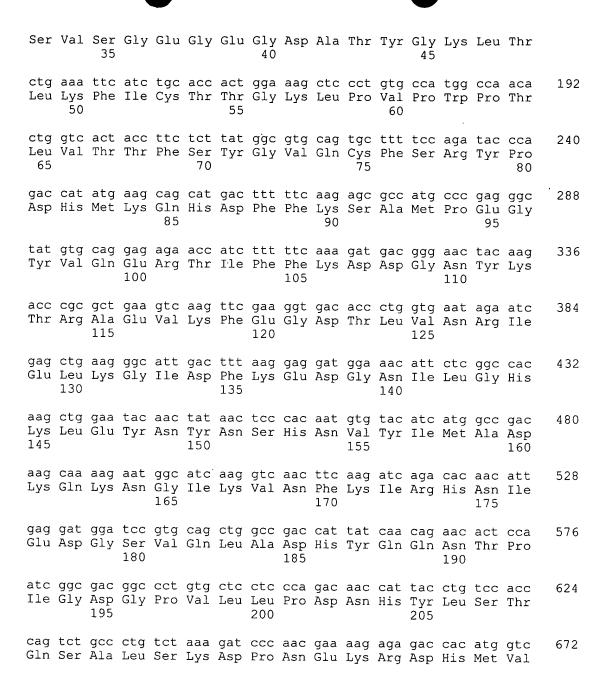
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gtc	cca	att	ctc	gtg	gaa	ctg	gat	ggc	gat	gtg	aat	ggg	cac	aaa	ttt	96



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Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His

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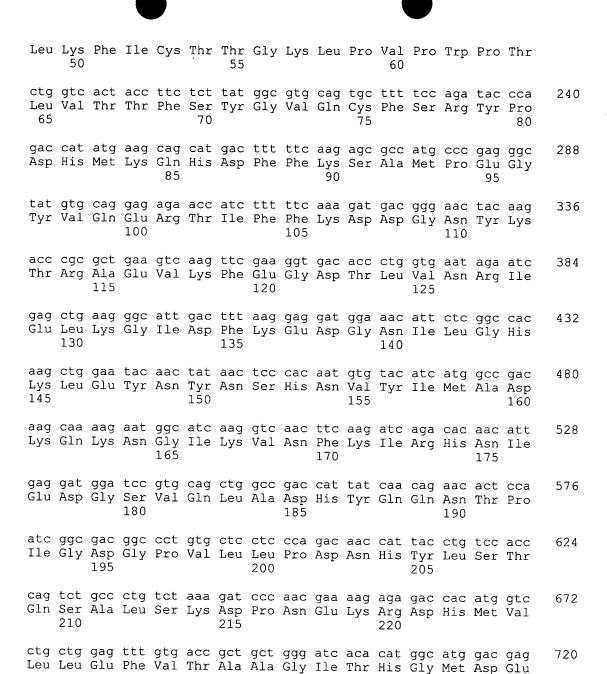


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Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val	
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gtc (Val 1	cca Pro	att Ile	ctc Leu 20	gtg Val	gaa Glu	ctg Leu	gat Asp	ggc Gly 25	gat Asp	gtg Val	aat Asn	ggg Gly	cac His 30	aaa Lys	ttt Phe	96
tct o	gtc Val	agc Ser 35	gga Gly	gag Glu	ggt Gly	gaa Glu	ggt Gly 40	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly 45	aag Lys	ctc Leu	acc Thr	14

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192



225 230 235 240

ctg tac aag tga Leu Tyr Lys 732

<210> 50

<211> 243

<212> PRT

<213> Artificial Sequence

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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

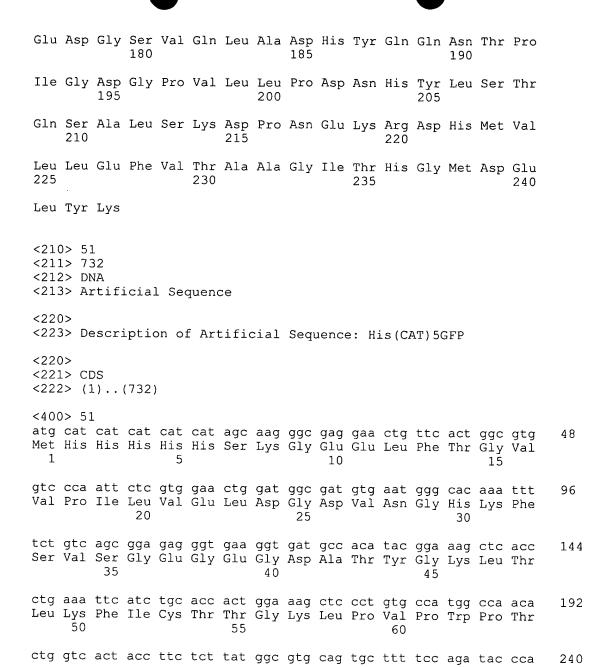
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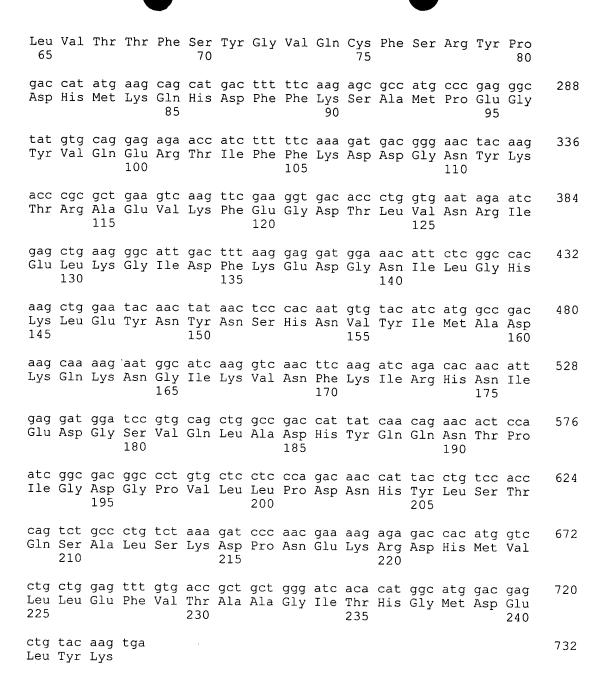
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175





<210> 52

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 52

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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

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Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

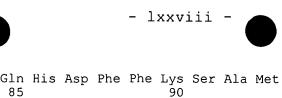
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Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr

195 200 205 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 215 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 235 Leu Tyr Lys <210> 53 <211> 732 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Ile(ATA)5GFP <220> <221> CDS <222> (1)..(732) <400> 53 atg ata ata ata ata agc aag ggc gag gaa ctg ttc act ggc gtg 48 Met Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 55 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc

288



Asp	His	Met	Ļys	Gln 85	His	Asp	Phe	Phe	Lys 90	Ser	Ala	Met	Pro	Glu 95	Gly	
														tac Tyr		336
														aga Arg		384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528
gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc Ile	ggc Gly	gac Asp 195	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	ggg Gly	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
	tac Tyr		tga													732

<210> 54 <211> 243 <212> PRT

<213> Artificial Sequence

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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

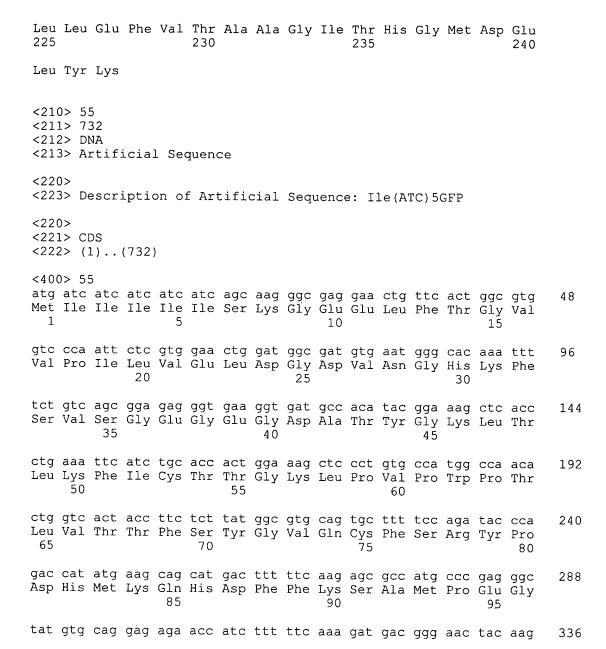
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Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220





Tyr	Val	Gln	Glu 100	Arg	Thr	Ile	Phe	Phe 105	Lys	Asp	Asp	Gly	Asn 110	Tyr	Lys	
acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggt Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528
gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc Ile	ggc Gly	gac Asp 195	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	ggg Gly	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
_	tac Tyr	aag Lys	tga	•												732

<210> 56 <211> 243 <212> PRT

<213> Artificial Sequence

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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

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Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

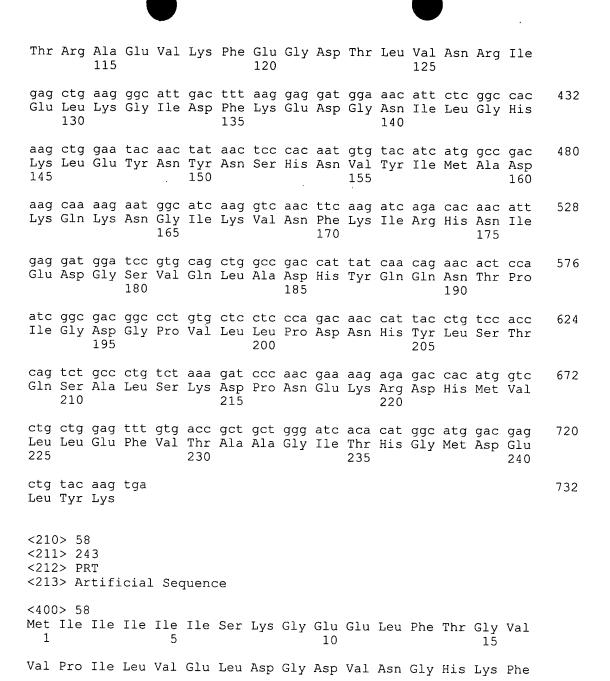
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Leu Tyr Lys

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gtc Val	cca Pro	att Ile	ctc Leu 20	gtg Val	gaa Glu	ctg Leu	gat Asp	ggc Gly 25	gat Asp	gtg Val	aat Asn	ggg Gly	cac His 30	aaa Lys	ttt Phe	96			
tct Ser	gtc Val	agc Ser 35	gga Gly	gag Glu	ggt Gly	gaa Glu	ggt Gly 40	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly 45	aag Lys	ctc Leu	acc Thr	144			
ctg Leu	aaa Lys 50	ttc Phe	atc Ile	tgc Cys	acc Thr	act Thr 55	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val 60	cca Pro	tgg Trp	cca Pro	aca Thr	192			
ctg Leu 65	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser 70	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys 75	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro 80	240			
gac Asp	cat His	atg Met	aag Lys	cag Gln 85	cat His	gac Asp	ttt Phe	ttc Phe	aag Lys 90	agc Ser	gcc Ala	atg Met	ccc Pro	gag Glu 95	ggc Gly	288			
cat Tyr	gtg Val	cag Gln	gag Glu 100	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	ggg Gly	aac Asn 110	tac Tyr	aag Lys	336			

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384



30

25

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 60

20

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

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Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

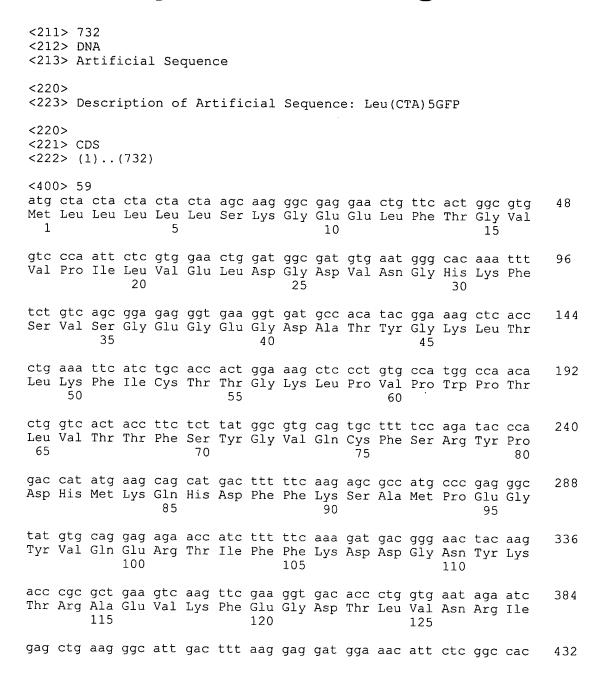
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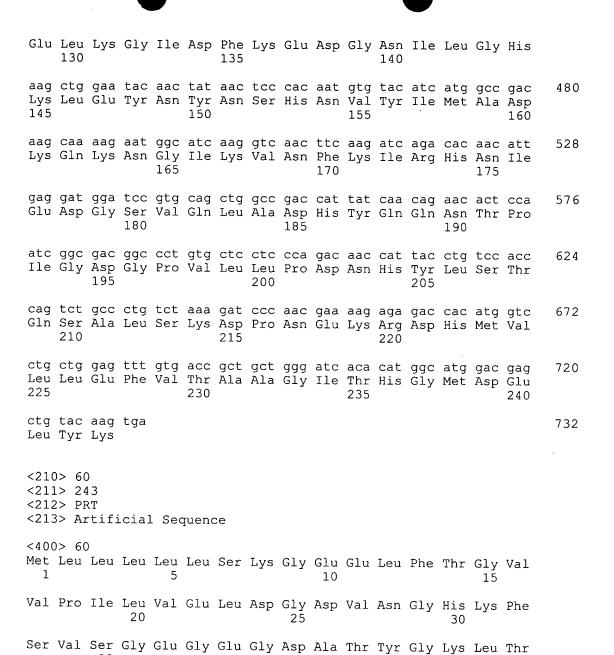
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Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 235 240

Leu Tyr Lys

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Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 . 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

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Leu Tyr Lys

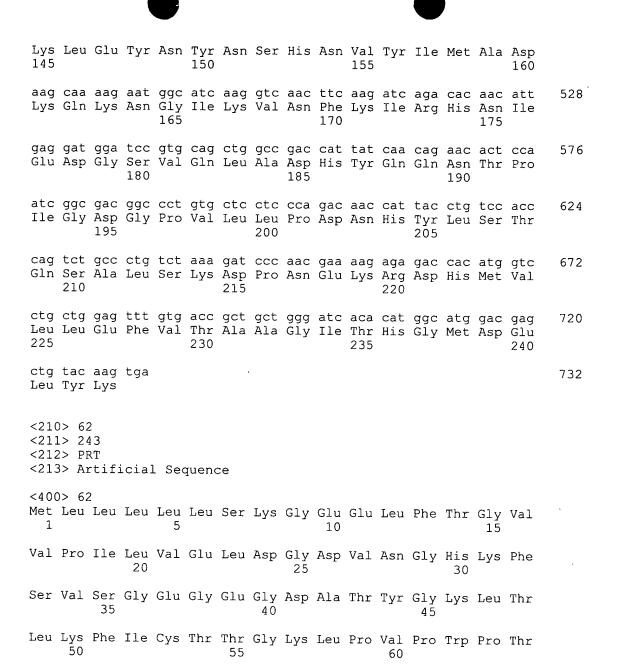
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Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

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Leu Tyr Lys

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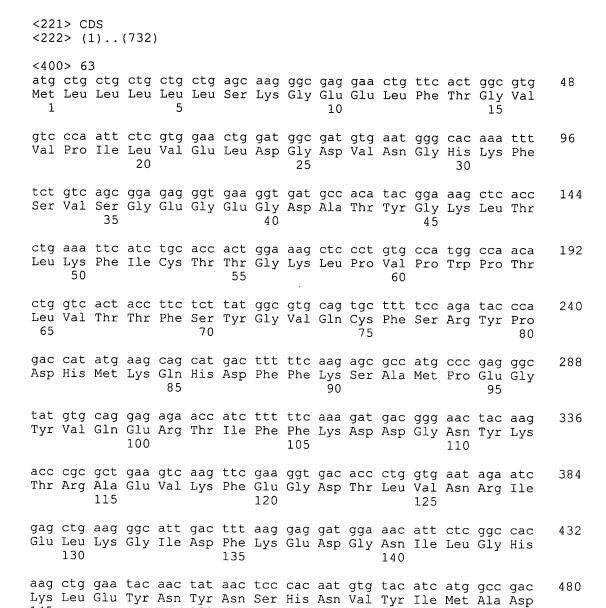
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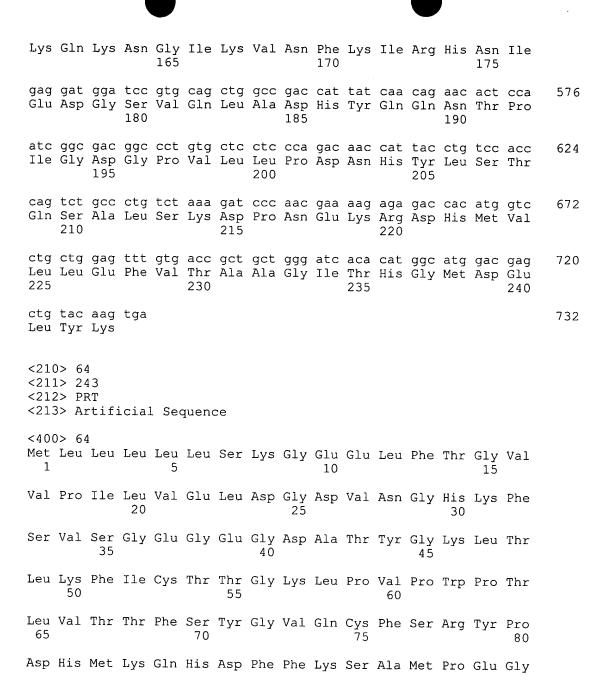
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528



85 90

95

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Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 120

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 135

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 155

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 185

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 200

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Leu Tyr Lys

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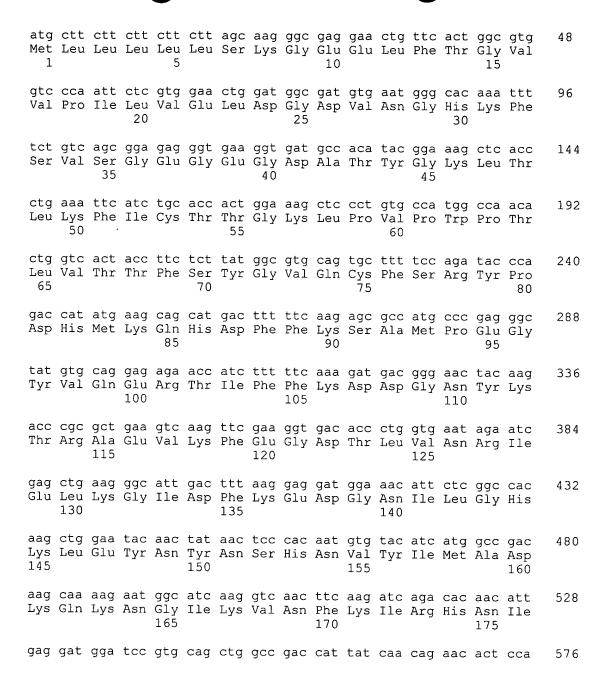
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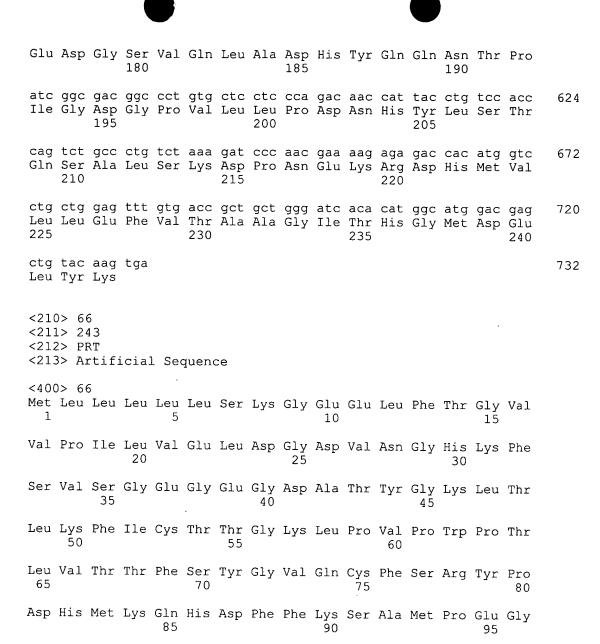
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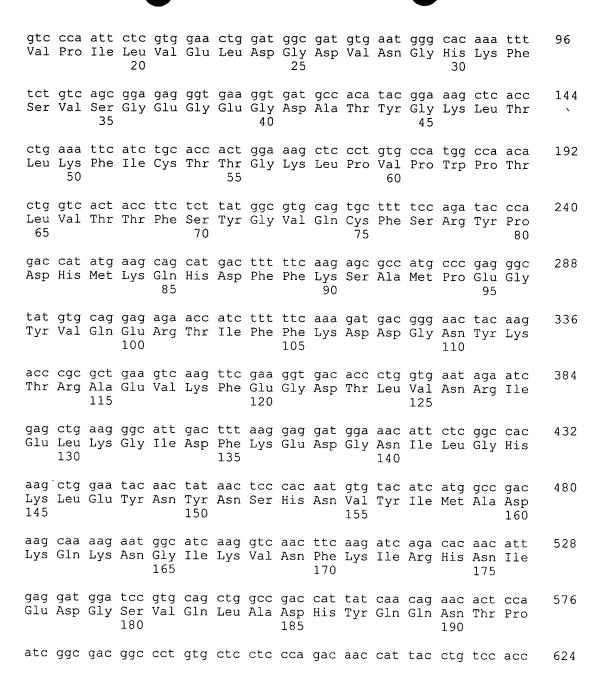
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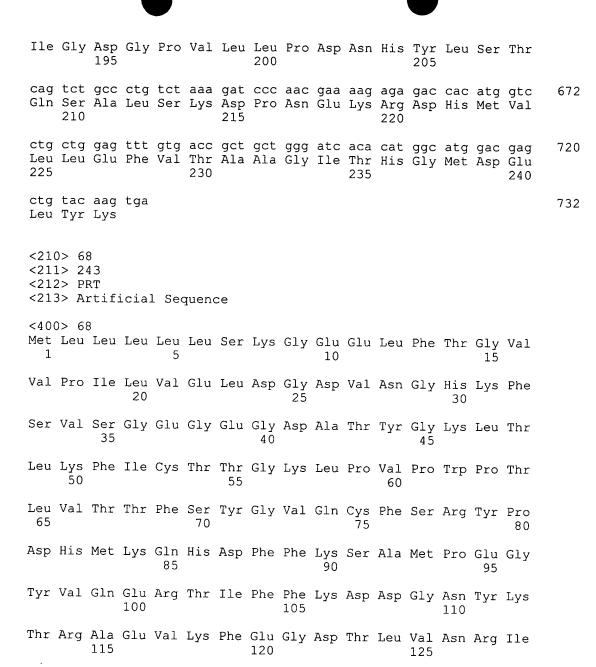
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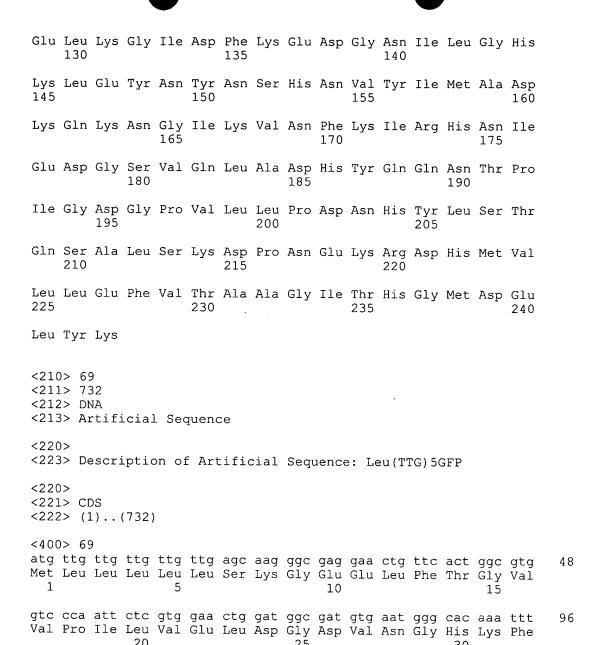
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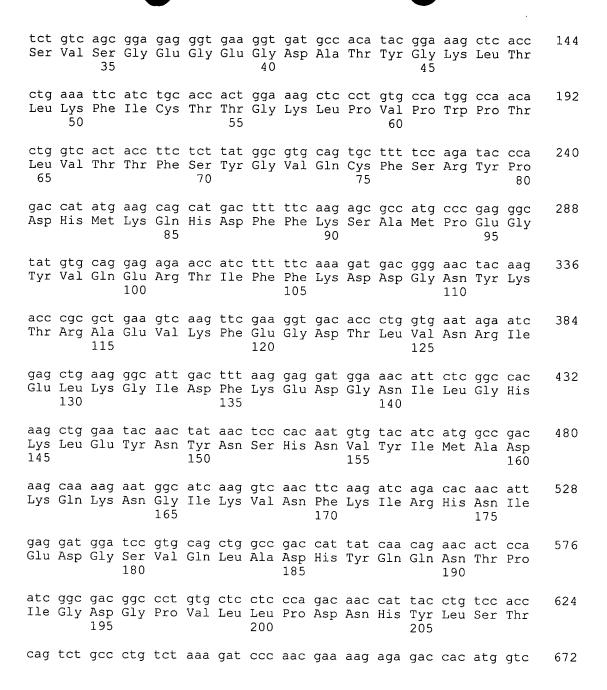
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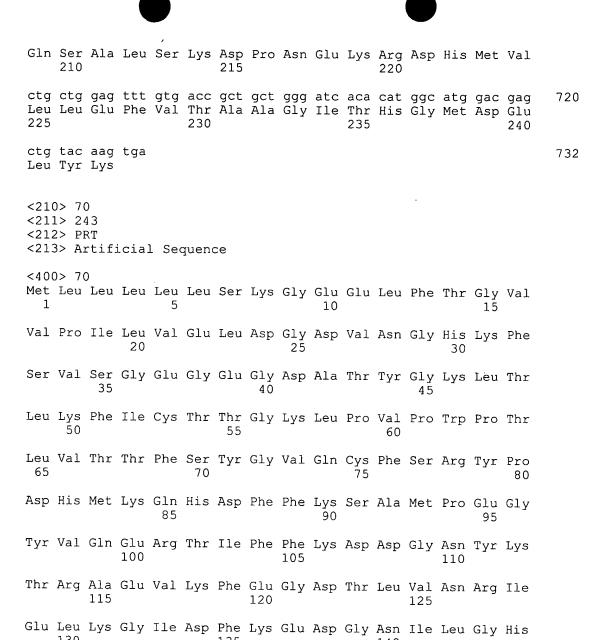
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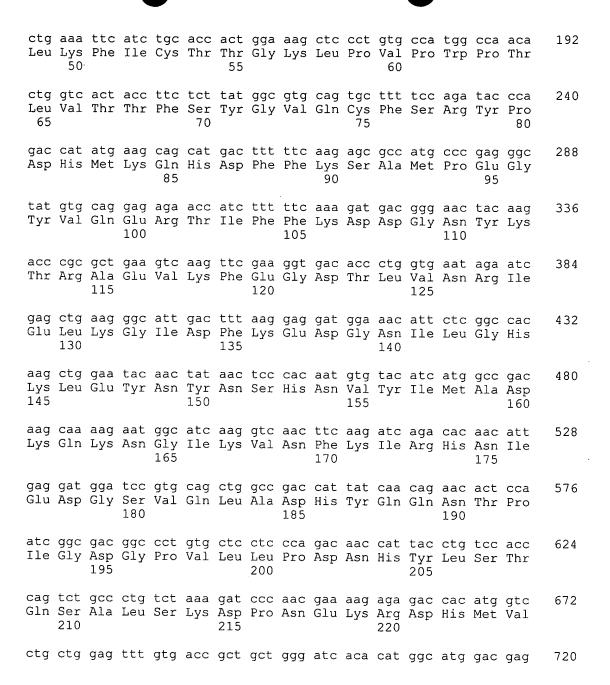


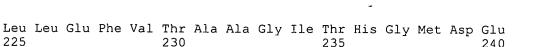




Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp

145					150					155		160				
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Glu Z	Asp	Gly	Ser 180	Val	Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro	
Ile	Gly	Asp 195	Gly	Pro	Val	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr	
Gln :	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val	
Leu 1 225	Leu	Glu	Phe	Val	Thr 230	Ala	Ala	Gly	Ile	Thr 235	His	Gly	Met	Asp	Glu 240	
Leu :	Tyr	Lys														
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gt <u>c</u> c	cca Pro	att Ile	ctc Leu 20	gtg Val	gaa Glu	ctg Leu	gat Asp	ggc Gly 25	gat Asp	gtg Val	aat Asn	ggg Gly	cac His 30	aaa Lys	ttt Phe	96
tct o	gtc Val	agc Ser 35	gga Gly	gag Glu	ggt Gly	gaa Glu	ggt Gly 40	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly 45	aag Lys	ctc Leu	acc Thr	144





ctg tạc aag tga Leu Tyr Lys 732

<210> 72

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 72

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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

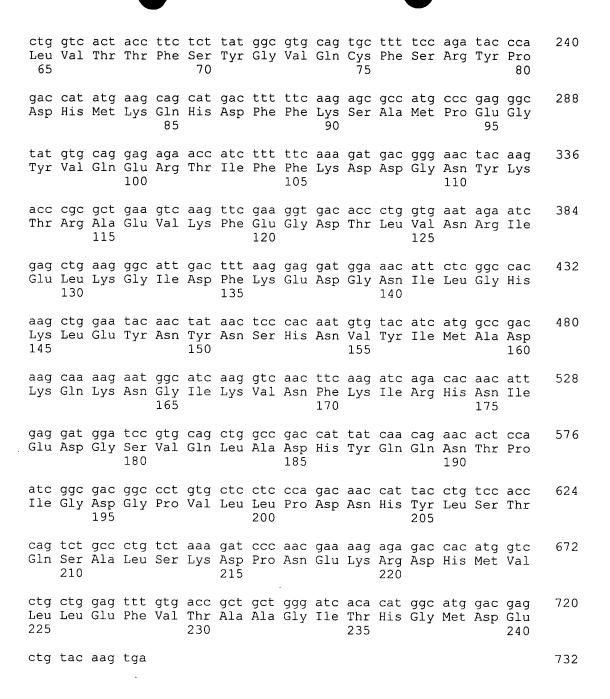
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Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu	Asp	Gly	Ser 180	Val	Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro	
Ile	Gly	Asp 195	Gly	Pro	Val	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr	
Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val	
Leu 225	Leu	Glu	Phe	Val	Thr 230	Ala	Ala	Gly	Ile	Thr 235	His	Gly	Met	Asp	Glu 240	
Leu	Tyr	Lys														
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gtc Val	cca Pro	att Ile	ctc Leu 20	gtg Val	gaa Glu	ctg Leu	gat Asp	ggc Gly 25	gat Asp	gtg Val	aat Asn	ggg Gly	cac His 30	aaa Lys	ttt Phe	96
tct Ser	gtc Val	agc Ser 35	gga Gly	gag Glu	ggt Gly	gaa Glu	ggt Gly 40	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly 45	aag Lys	ctc Leu	acc Thr	144
ctg Leu	aaa Lys 50	ttc Phe	atc Ile	tgc Cys	acc Thr	act Thr 55	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val 60	cca Pro	tgg Trp	cca Pro	aca Thr	192



Leu Tyr Lys

<210> 74

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 74

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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

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Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

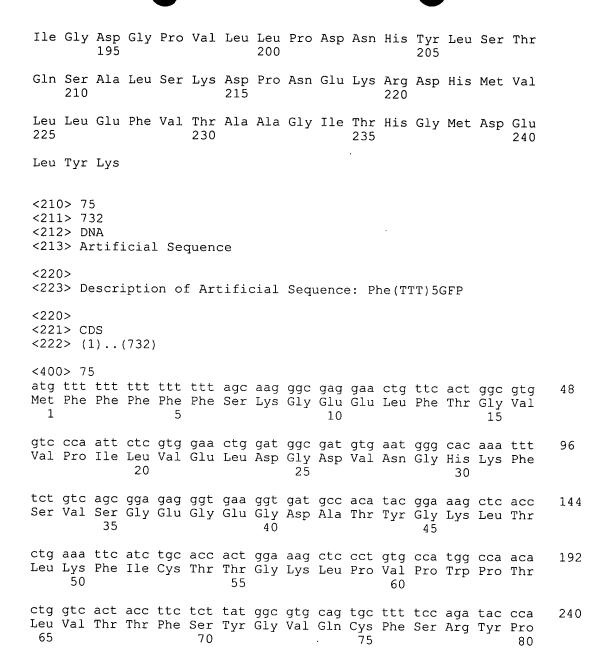
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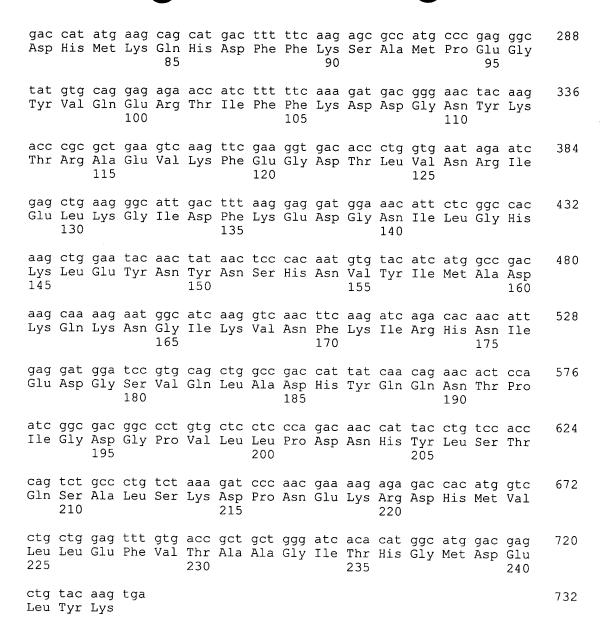
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Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190





<210> 76

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 76 .

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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly. Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

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Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val

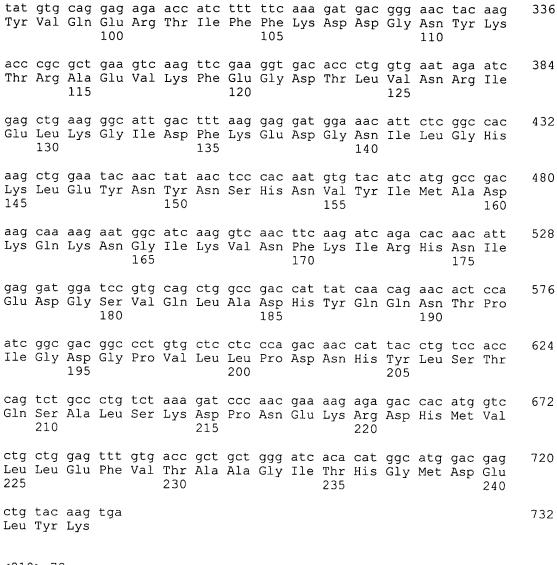
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Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly

90

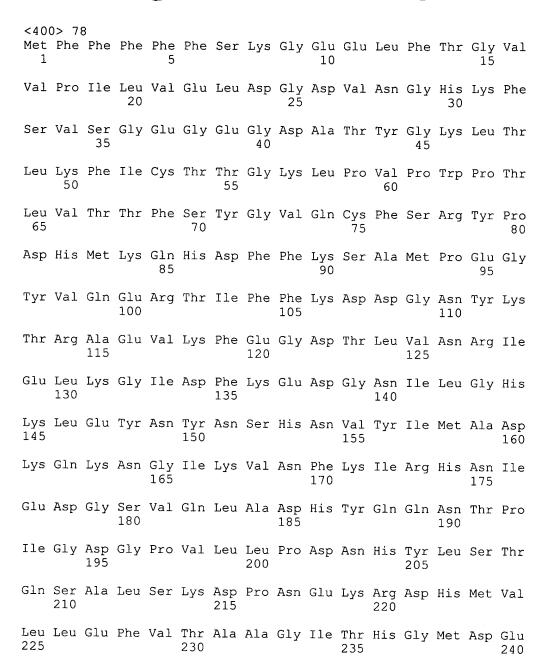


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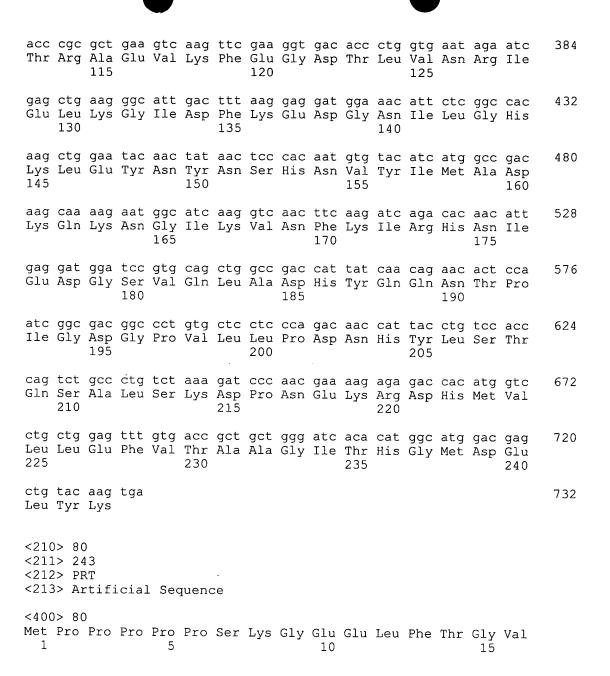
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Leu Tyr Lys

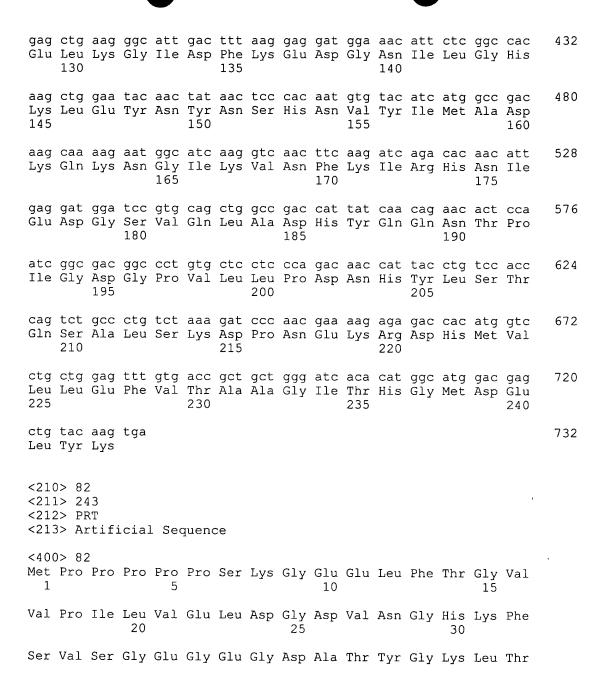
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Leu Tyr Lys

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 105 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 135 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 170 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 185 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 200 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu

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gtc Val	cca Pro	att Ile	ctc Leu 20	gtg Val	gaa Glu	ctg Leu	gat Asp	ggc Gly 25	gat Asp	gtg Val	aat Asn	ggg Gly	cac His 30	aaa Lys	ttt Phe	96
tct Ser	gtc Val	agc Ser 35	gga Gly	gag Glu	ggt Gly	gaa Glu	ggt Gly 40	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly 45	aag Lys	ctc Leu	acc Thr	144
ctg Leu	aaa Lys 50	ttc Phe	atc Ile	tgc Cys	acc Thr	act Thr 55	gga Gly	aag Lys	ctc Leu	cct Pro	gtg Val 60	cca Pro	tgg Trp	cca Pro	aca Thr	192
ctg Leu 65	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser 70	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys 75	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro 80	240
gac Asp	cat His	atg Met	aag Lys	cag Gln 85	cat His	gac Asp	ttt Phe	ttc Phe	aag Lys 90	agc Ser	gcc Ala	atg Met	ccc Pro	gag Glu 95	ggc Gly	288
tat Tyr	gtg Val	cag Gln	gag Glu 100	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	ggg Gly	aac Asn 110	tac Tyr	aag Lys	336
acc Thr	cgc Arg	gct Ala 115	gaa Glu	gtc Val	aag Lys	ttc Phe	gaa Glu 120	ggt Gly	gac Asp	acc Thr	ctg Leu	gtg Val 125	aat Asn	aga Arg	atc Ile	384



35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

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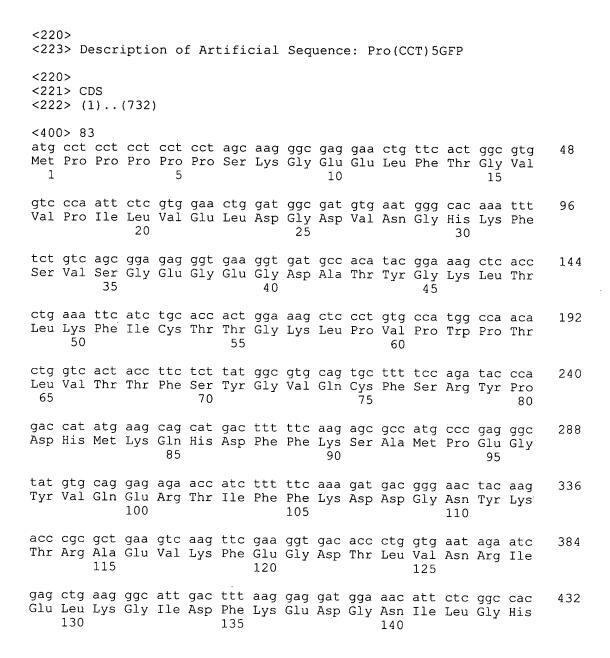
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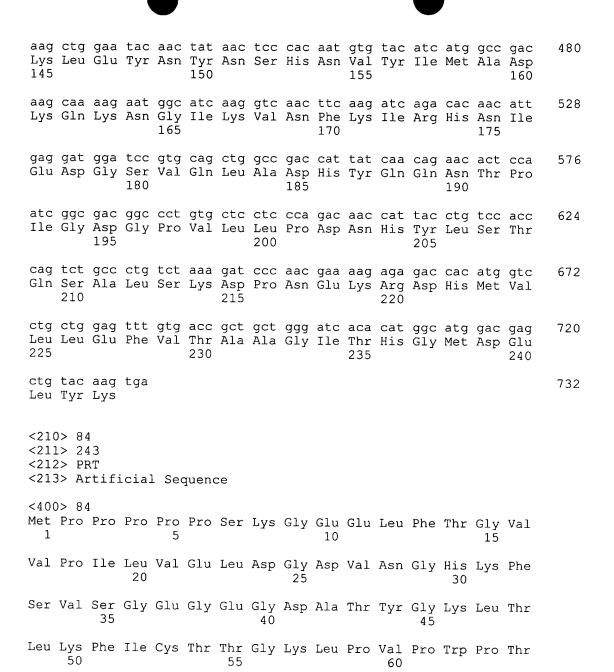
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Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

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Leu Tyr Lys

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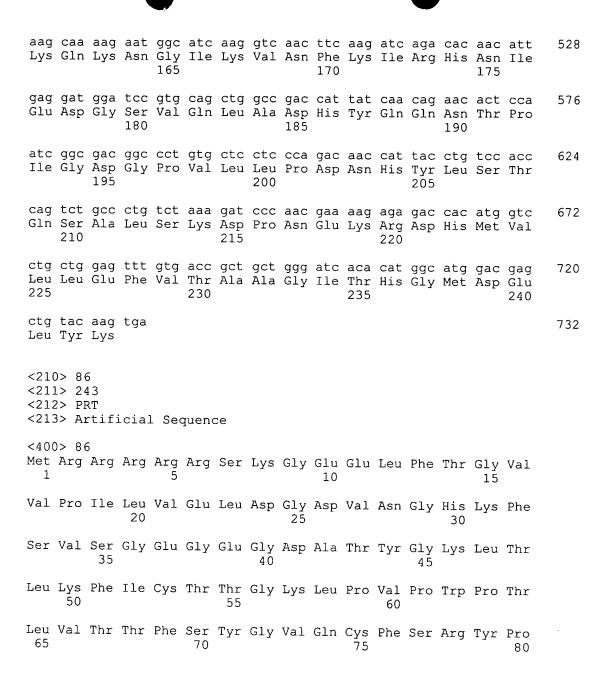
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Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr $195 \hspace{1cm} 200 \hspace{1cm} 205 \hspace{1cm}$

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Leu Tyr Lys

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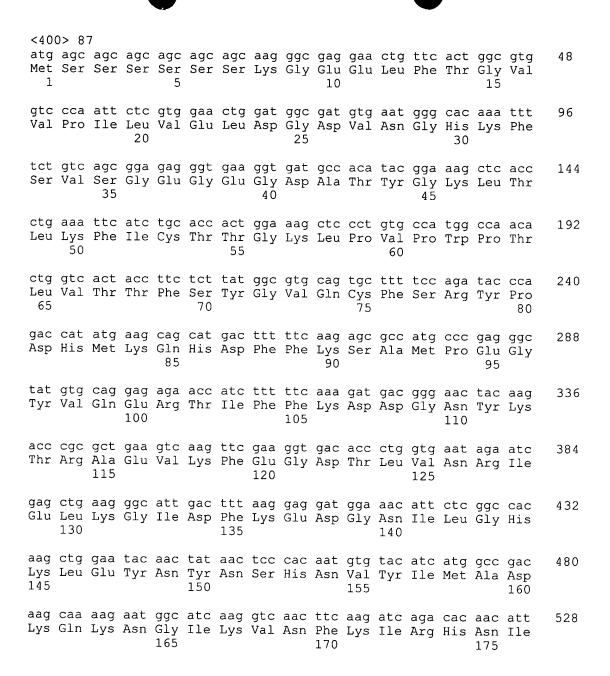
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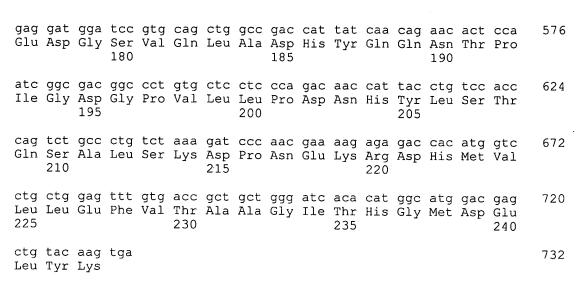
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Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 55

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Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly

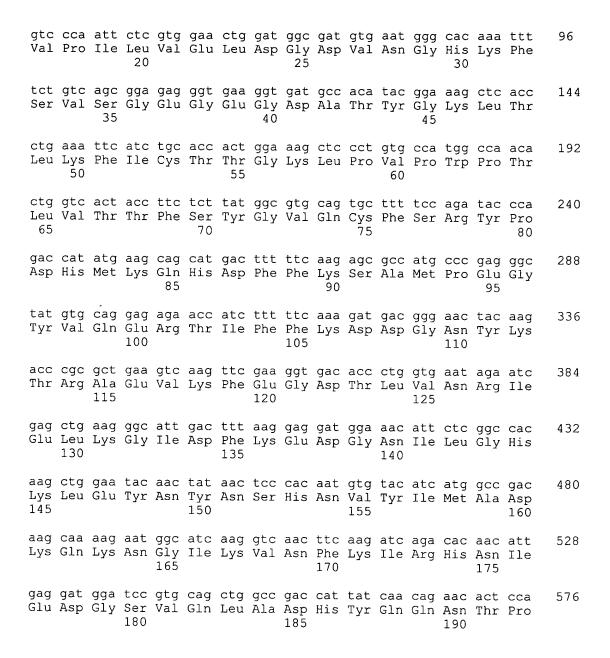
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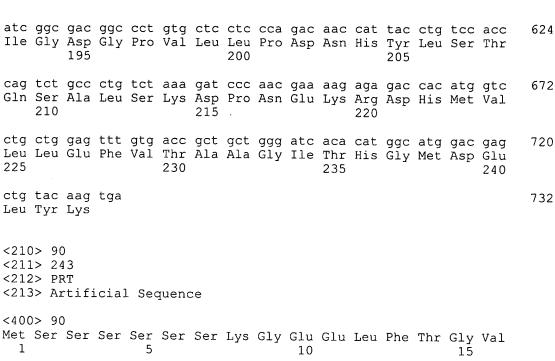
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Glu Leu Lys 130	Gly Ile A	Asp Phe Lys 135	Glu Asp Gly	Asn Ile I	Leu Gly His										
Lys Leu Glu 145	Tyr Asn 1	Tyr Asn Ser 150	His Asn Val 155	Tyr Ile M	Met Ala Asp 160										
Lys Gln Lys	Asn Gly 1 165	Ile Lys Val	Asn Phe Lys 170	Ile Arg H	His Asn Ile 175										
Glu Asp Gly	Ser Val (Gln Leu Ala	Asp His Tyr 185		Asn Thr Pro										
Ile Gly Asp 195	Gly Pro \	Val Leu Leu 200	Pro Asp Asn	His Tyr I 205	Leu Ser Thr										
Gln Ser Ala 210	Leu Ser I	Lys Asp Pro 215	Asn Glu Lys	Arg Asp H	His Met Val										
Leu Leu Glu 225	Phe Val 7	Thr Ala Ala 230	Gly Ile Thr 235	His Gly M	Met Asp Glu 240										
Leu Tyr Lys	Leu Tyr Lys														
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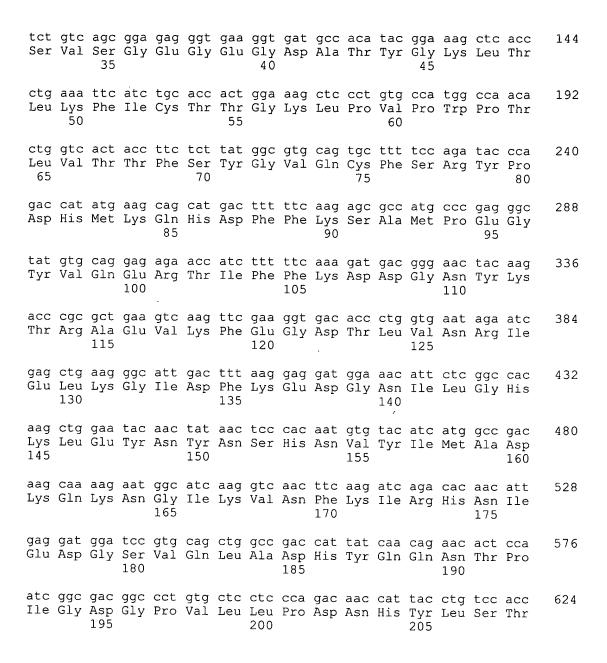
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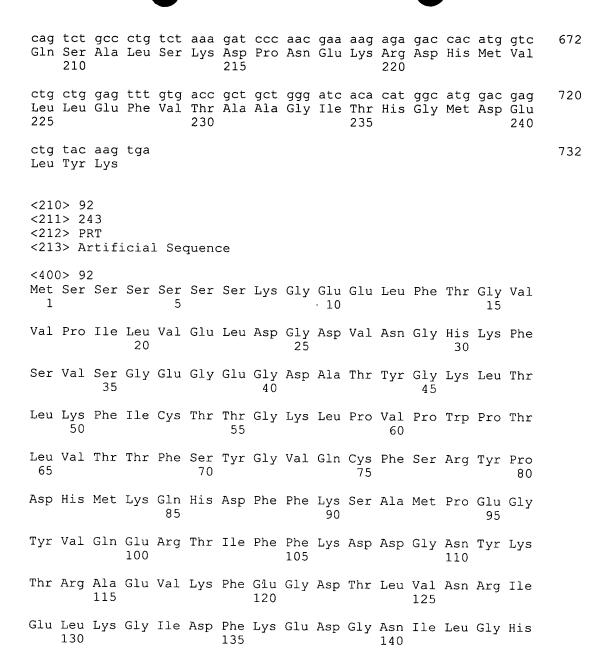
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1 5 10 15



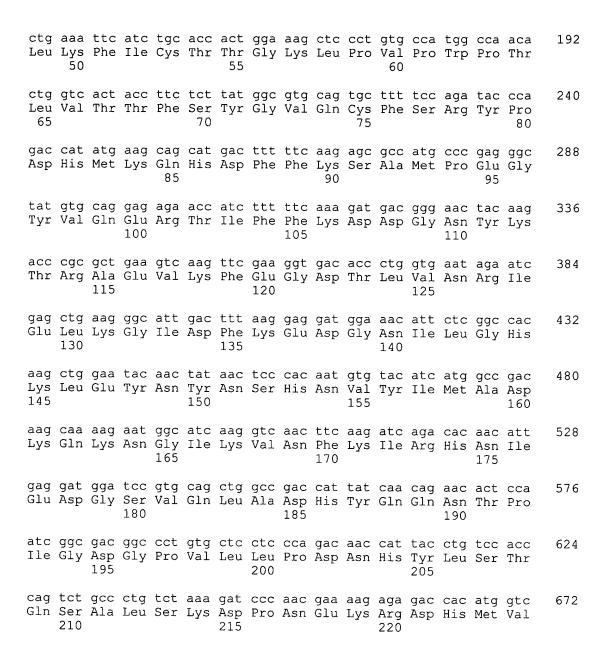


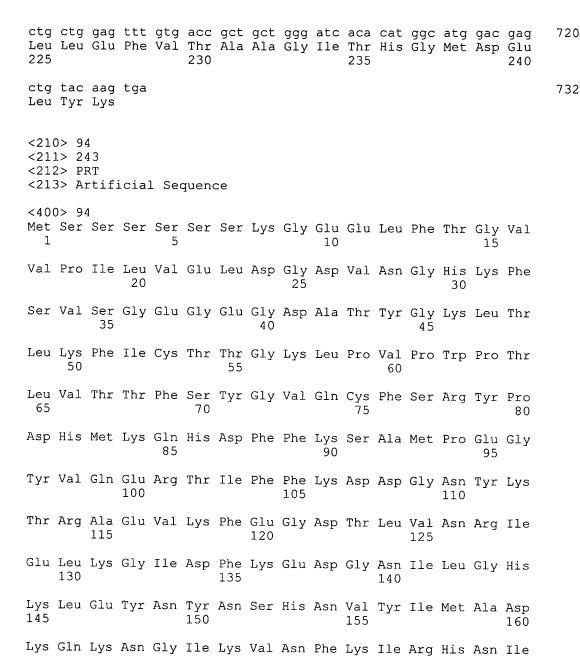
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 185 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 200 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 230 235 Leu Tyr Lys <210> 91 <211> 732 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Ser(TCA)5GFP <220> <221> CDS <222> (1)..(732) <400> 91 atg tca tca tca tca agc aag ggc gag gaa ctg ttc act ggc gtg Met Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val 10 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe





Lys 145	Leu	Glu	Tyr	Asn	Tyr 150	Asn	Ser	His	Asn	Val 155	Tyr	Ile	Met	Ala	Asp 160	
Lys	Gln	Lys	Asn	Gly 165	Ile	Lys	Val	Asn	Phe 170	Lys	Ile	Arg	His	Asn 175	Ile	
Glu	Asp	Gly	Ser 180	Val	Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro	
Ile	Gly	Asp 195	Gly	Pro	Val	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr	
Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val	
Leu 225	Leu	Glu	Phe	Val	Thr 230	Ala	Ala	Gly	Ile	Thr 235	His	Gly	Met	Asp	Glu 240	
Leu	Leu Tyr Lys															
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gtc Val	cca Pro	att Ile	ctc Leu 20	gtg Val	gaa Glu	ctg Leu	gat Asp	ggc Gly 25	gat Asp	gtg Val	aat Asn	ggg Gly	cac His 30	aaa Lys	ttt Phe	96
tct Ser	gtc Val	agc Ser 35	gga Gly	gag Glu	ggt Gly	gaa Glu	ggt Gly 40	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly 45	aag Lys	ctc Leu	acc Thr	14

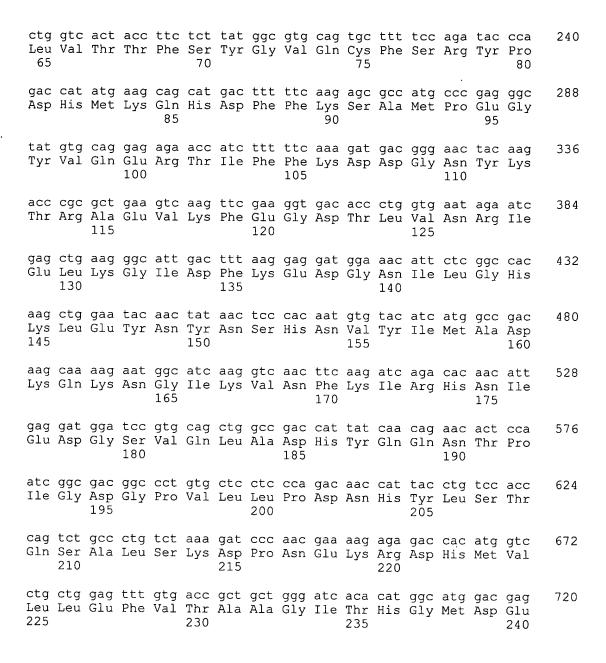




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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr

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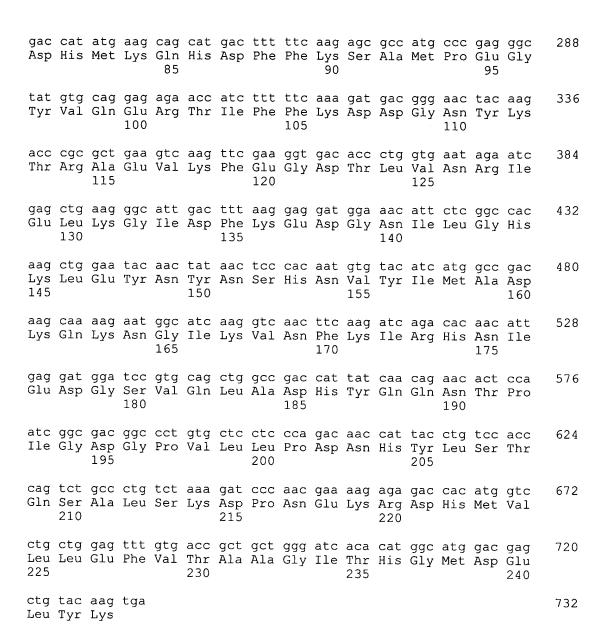


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Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr
Leu	Lys 50	Phe	Ile	Суѕ	Thr	Thr 55	Gly	Lys	Leu	Pro	Val 60	Pro	Trp	Pro	Thr
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Tyr	Val	Gln	Glu 100	Arg	Thr	Ile	Phe	Phe 105	Lys	Asp	Asp	Gly	Asn 110	Tyr	Lys
Thr	Arg	Ala 115	Glu	Val	Lys	Phe	Glu 120	Gly	Asp	Thr	Leu	Val 125	Asn	Arg	Ile
Glu	Leu 130	Lys	Gly	Ile	Asp	Phe 135	Lys	Glu	Asp	Gly	Asn 140	Ile	Leu	Gly	His
Lys 145	Leu	Glu	Tyr	Asn	Tyr 150	Asn	Ser	His	Asn	Val 155	Tyr	Ile	Met	Ala	Asp 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro

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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

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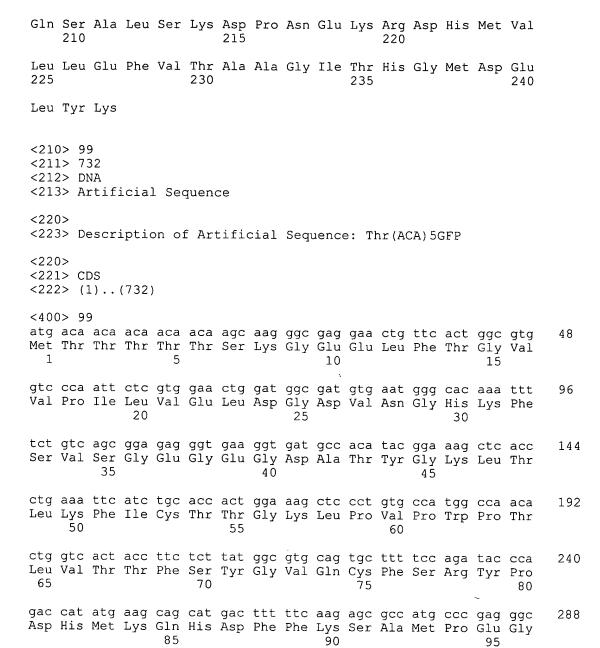
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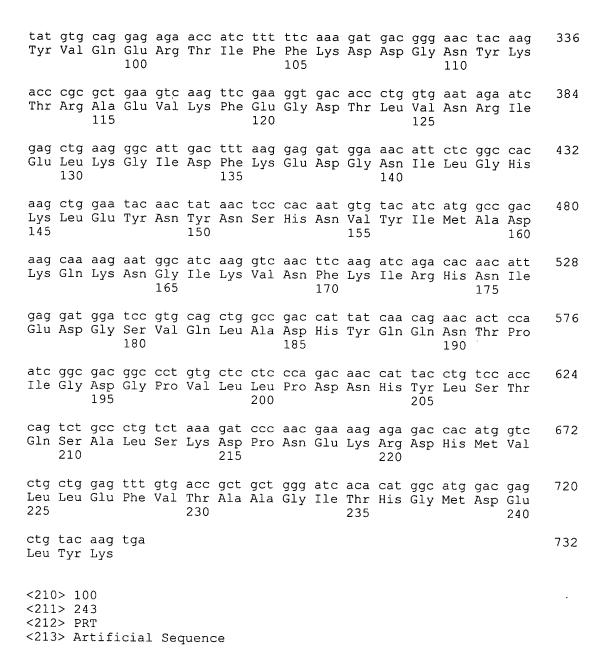
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Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

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Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205





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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

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Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 45

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ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65

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Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 95

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Tyr Val Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
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aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
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gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
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Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

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Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

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Leu Tyr Lys

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Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

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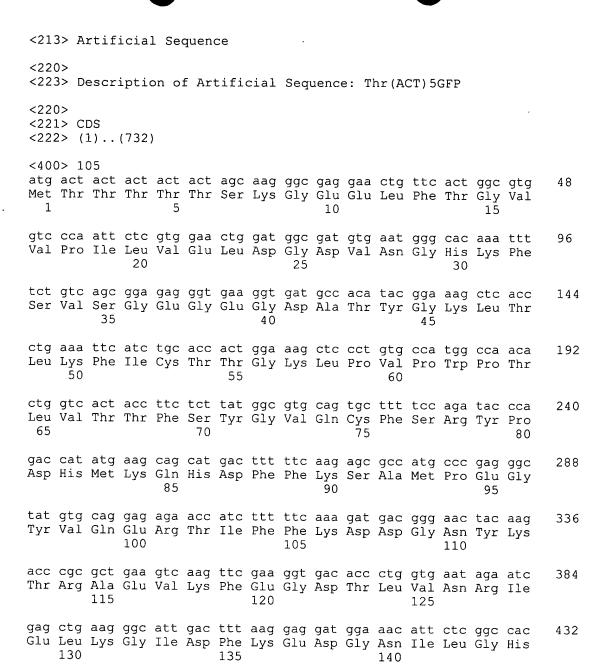
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Leu Tyr Lys

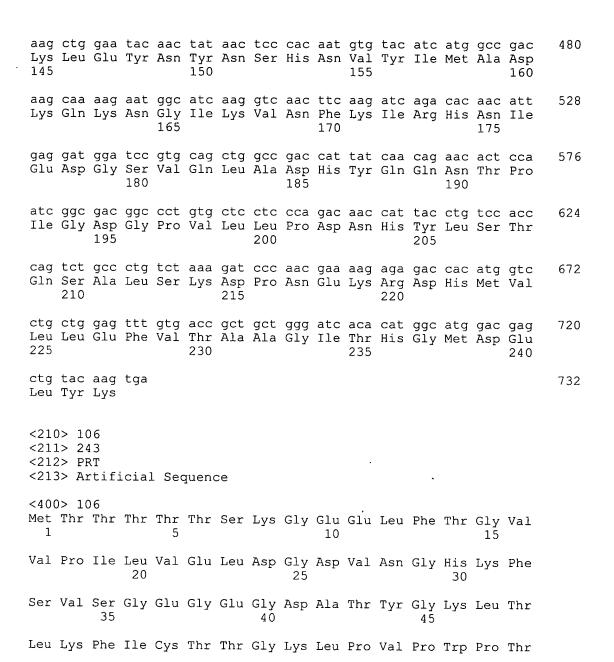
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Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

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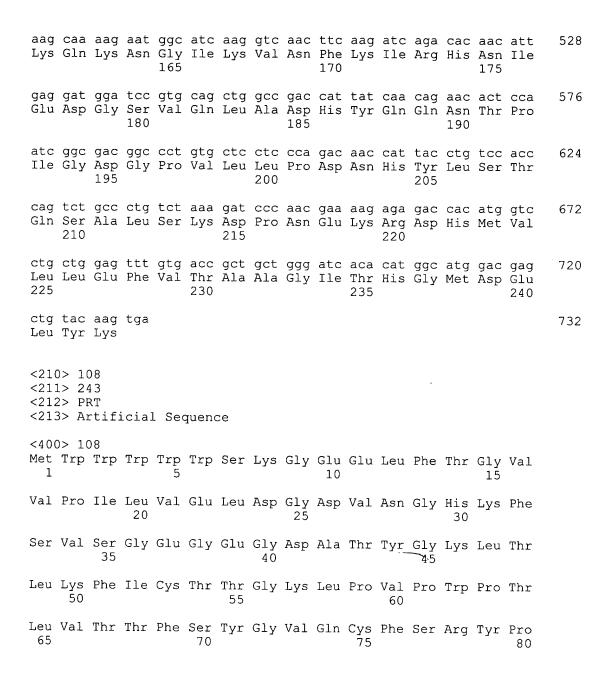
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Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
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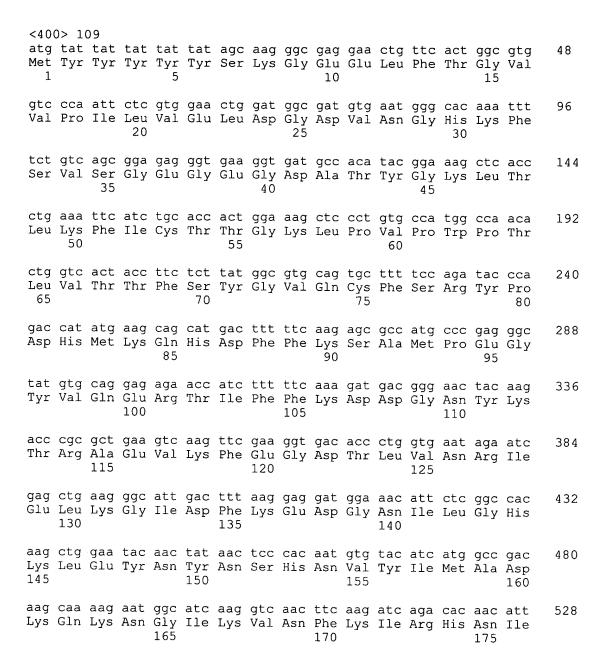
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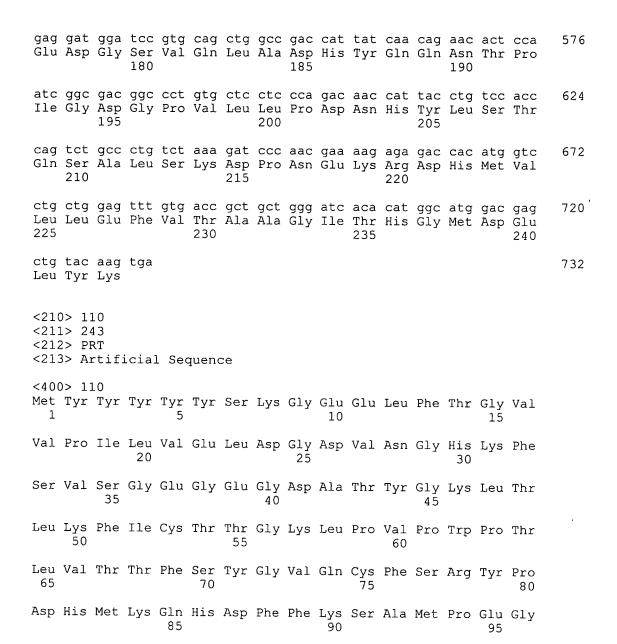
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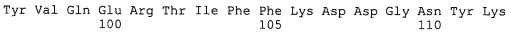
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Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

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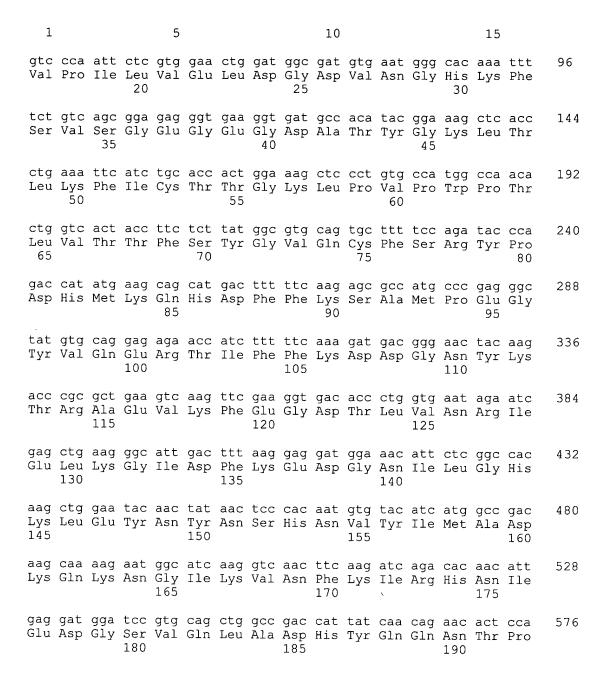
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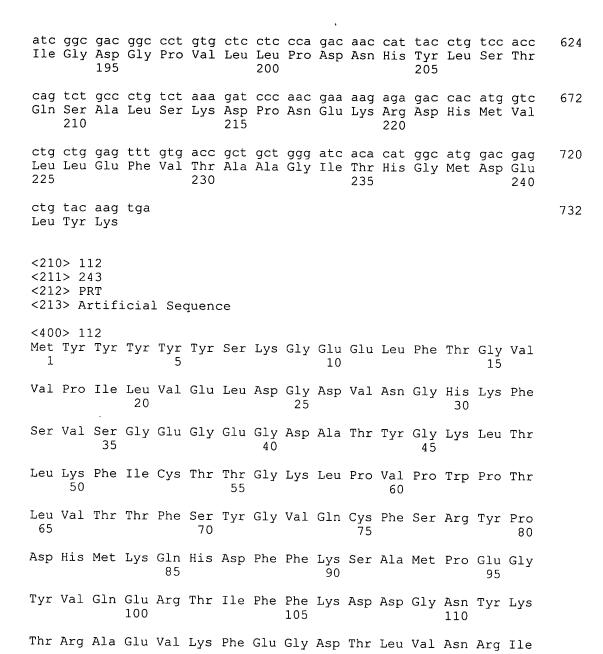
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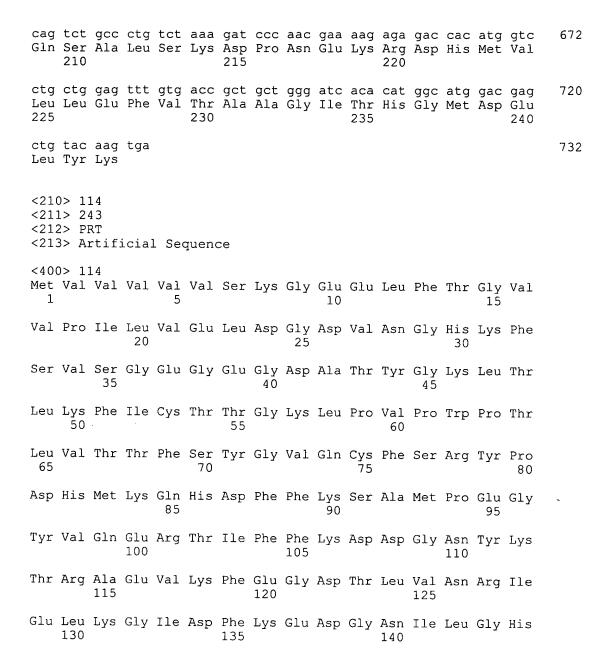
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Glu Leu Lys 130	Gly Ile As	p Phe Lys 135	Glu Asp Gl	ly Asn Ile L 140	eu Gly His									
Lys Leu Glu 145	Tyr Asn Ty 15		His Asn Va	al Tyr Ile M 55	et Ala Asp 160									
Lys Gln Lys	Asn Gly Il 165	e Lys Val	Asn Phe Ly 170	/s Ile Arg H	is Asn Ile 175									
Glu Asp Gly	Ser Val Gl 180	n Leu Ala	Asp His Ty 185	yr Gln Gln A 1	sn Thr Pro 90									
Ile Gly Asp 195	Gly Pro Va	l Leu Leu 200	Pro Asp As	sn His Tyr L 205	eu Ser Thr									
Gln Ser Ala 210	Leu Ser Ly	s Asp Pro 215	Asn Glu Ly	s Arg Asp H 220	is Met Val									
Leu Leu Glu 225	Phe Val Th		Gly Ile Th	nr His Gly M B5	et Asp Glu 240									
Leu Tyr Lys														
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gtc cca att Val Pro Ile	ctc gtg ga Leu Val Gl	ctg gat Leu Asp	ggc gat gte Gly Asp Va	g aat ggg c	ac aaa ttt 96 is Lys Phe									

30

25

20

tet gte age gga gag ggt gaa ggt gat gee aca tae gga aag ete ace 144 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 70 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 8.5 90 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 120 gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 135 aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 150 155 aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 170 gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 185 atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624 Ile Gly Asp Gly Pro Val Leu Pro Asp Asn His Tyr Leu Ser Thr

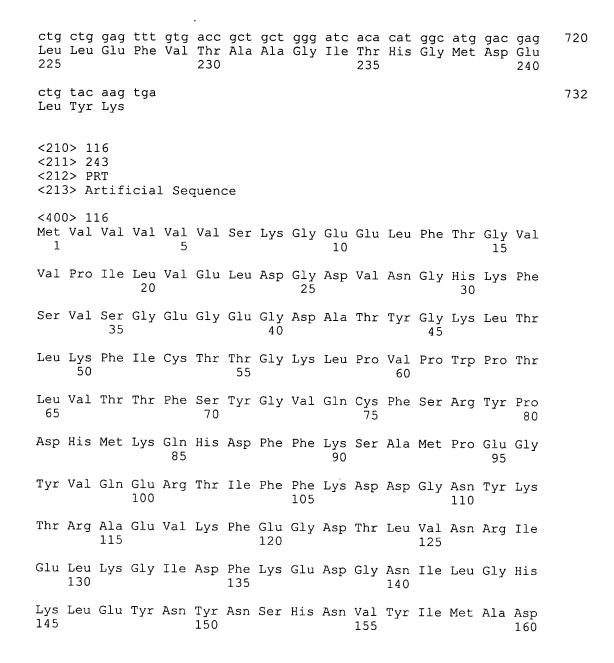


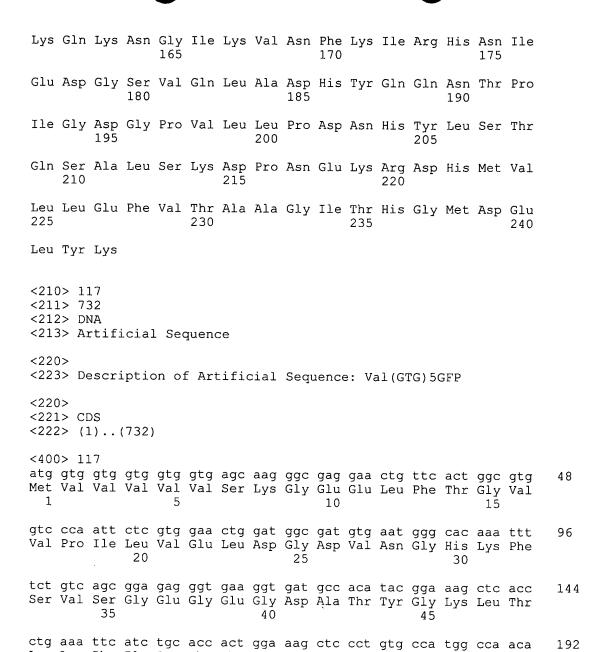
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Lys	Gln	Lys	Asn	Gly 165	Ile	Lys	Val	Asn	Phe 170	Lys	Ile	Arg	His	Asn 175	Ile	
Glu	Asp	Gly	Ser 180	Val	Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro	
Ile	Gly	Asp 195	Gly	Pro	Val [.]	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr	
Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val	
Leu 225	Leu	Glu	Phe	Val	Thr 230	Ala	Ala	Gly	Ile	Thr 235	His	Gly	Met	Asp	Glu 240	
Leu	Tyr	Lys														
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gtc Val	cca Pro	att Ile	ctc Leu 20	gtg Val	gaa Glu	ctg Leu	gat Asp	ggc Gly 25	gat Asp	gtg Val	aat Asn	gly	cac His 30	aaa Lys	ttt Phe	96
tct Ser	gtc Val	agc Ser	gga Gly	gag Glu	ggt Gly	gaa Glu	ggt Gly	gat Asp	gcc Ala	aca Thr	tac Tyr	gga Gly	aag Lys	ctc Leu	acc Thr	14

144



35 40 45 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 7.0 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 105 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 135 aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 150 155 aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 185 atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 200 cag tot goo etg tot aaa gat ooc aac gaa aag aga gac cac atg gto 672 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val





Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr

192

60

55

50

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 70 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 105 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 135 aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 155 aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 215 ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu

ctg tac aag tga Leu Tyr Lys

732

<210> 118

<211> 243

<212> PRT

<213> Artificial Sequence

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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro

180

185

190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 240

Leu Tyr Lys

<210> 119

<211> 732

<212> DNA

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<220> <221> CDS <222> (1)..(732)

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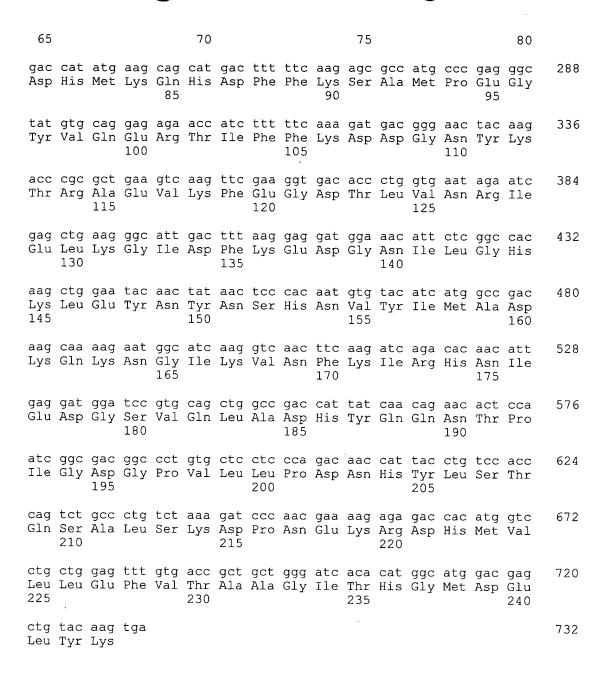
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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc $$ 144 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr $$ 35 $$ 40 $$ 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro



<210> 120

<211> 243

<212> PRT

<213> Artificial Sequence

<400> 120

Met Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val 1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

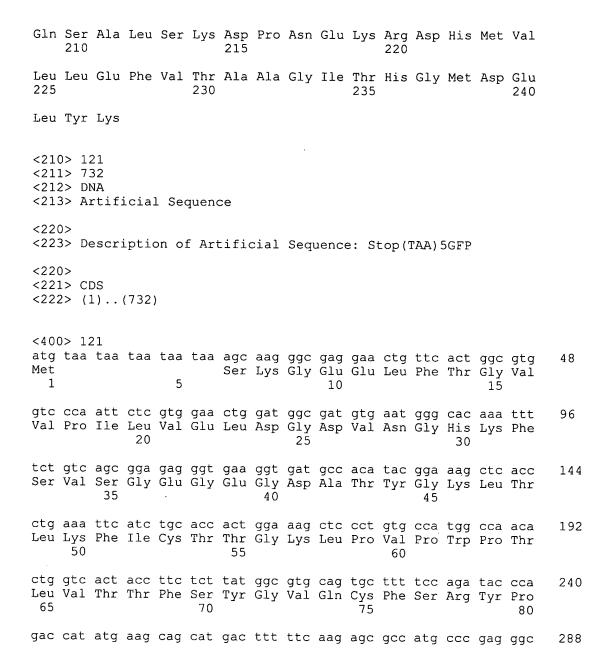
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

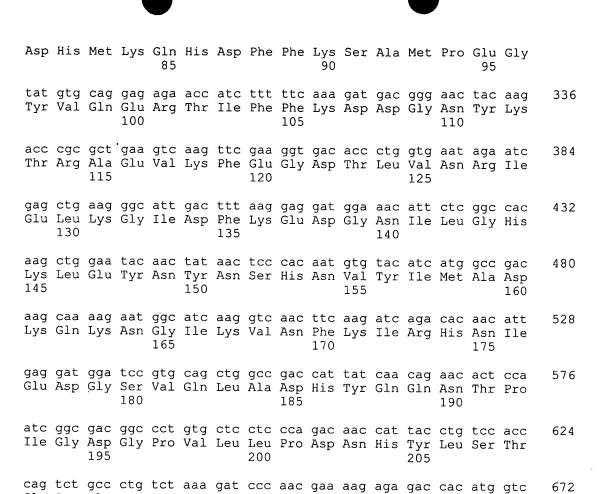
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Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205





Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val

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Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu

230

<210> 122 <211> 732

Leu Tyr Lys

225

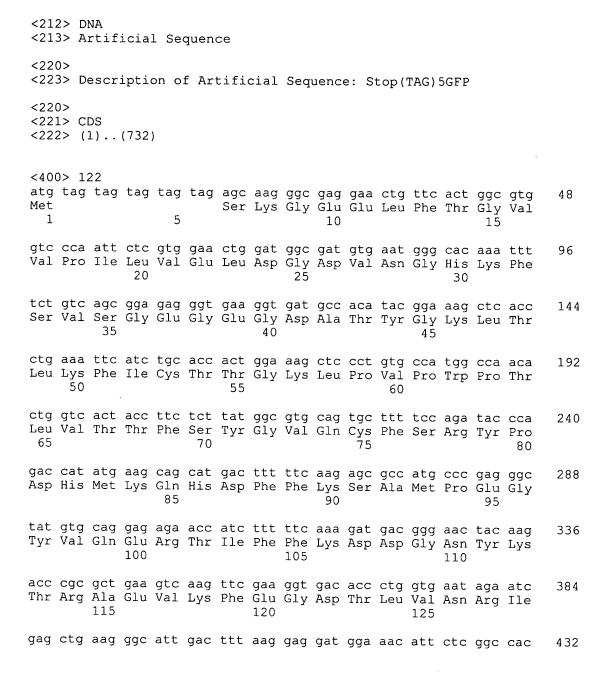
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ctg tac aag tga

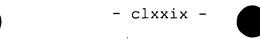
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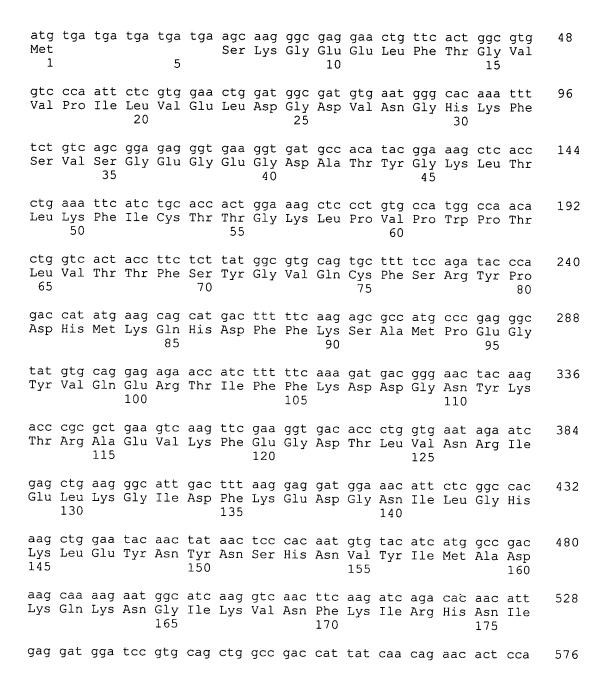
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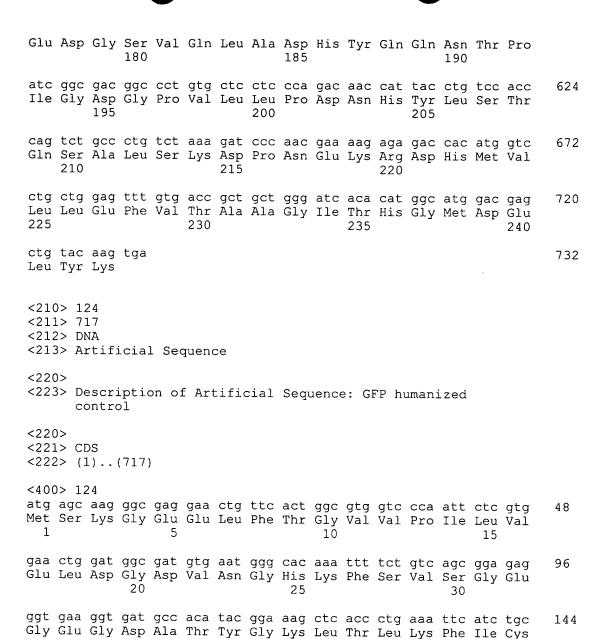


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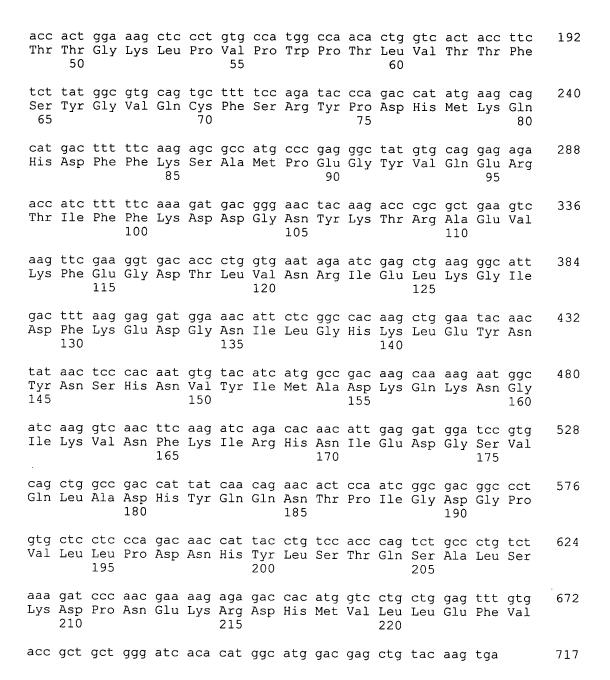


Glu	Leu 130	Lys	Gly	Ile	Asp	Phe 135	Lys	Glu	Asp	Gly	Asn 140	Ile	Leu	Gly	His	
aag Lys 145	ctg Leu	gaa Glu	tac Tyr	aac Asn	tat Tyr 150	aac Asn	tcc Ser	cac His	aat Asn	gtg Val 155	tac Tyr	atc Ile	atg Met	gcc Ala	gac Asp 160	480
aag Lys	caa Gln	aag Lys	aat Asn	ggc Gly 165	atc Ile	aag Lys	gtc Val	aac Asn	ttc Phe 170	aag Lys	atc Ile	aga Arg	cac His	aac Asn 175	att Ile	528
gag Glu	gat Asp	gga Gly	tcc Ser 180	gtg Val	cag Gln	ctg Leu	gcc Ala	gac Asp 185	cat His	tat Tyr	caa Gln	cag Gln	aac Asn 190	act Thr	cca Pro	576
atc Ile	ggc Gly	gac Asp 195	ggc Gly	cct Pro	gtg Val	ctc Leu	ctc Leu 200	cca Pro	gac Asp	aac Asn	cat His	tac Tyr 205	ctg Leu	tcc Ser	acc Thr	624
cag Gln	tct Ser 210	gcc Ala	ctg Leu	tct Ser	aaa Lys	gat Asp 215	ccc Pro	aac Asn	gaa Glu	aag Lys	aga Arg 220	gac Asp	cac His	atg Met	gtc Val	672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	ggg Gly	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
	tac Tyr		tga													732
<211 <212)> 12 .> 73 ?> DN 3> Ar	32 IA	cial	. Seç	luenc	e										
<220 <223		scri	.ptic	n of	Art	ific	ial	Sequ	ience	e: St	r) qo:	'GA) 5	GFP			•
)> .> CD !> (1		732)													





40



-

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys 225 230 235

<210> 125

<'211> 238

<212> PRT

<213> Artificial Sequence

<400> 125

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe 50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110

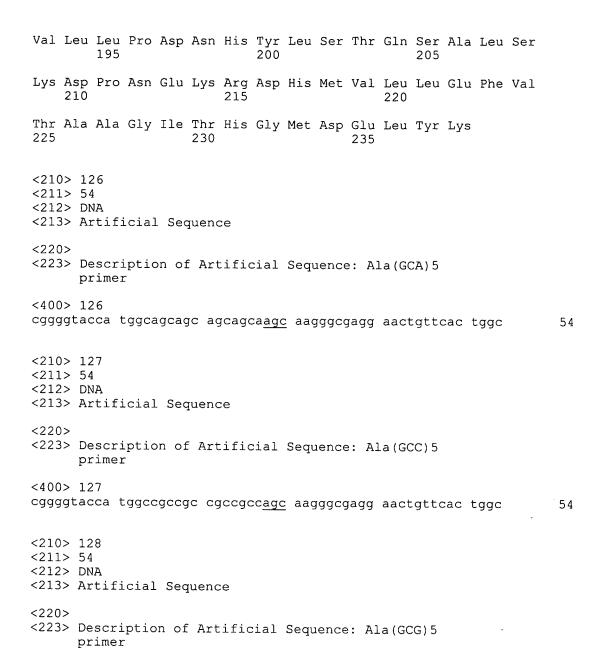
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125

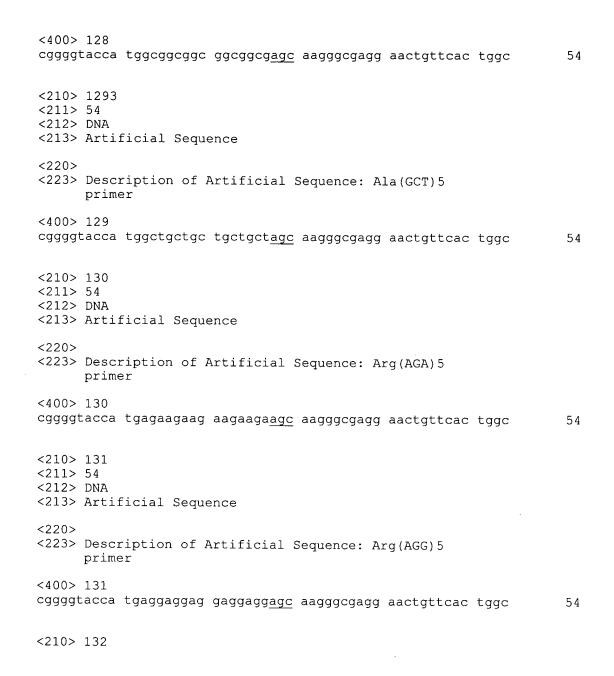
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140

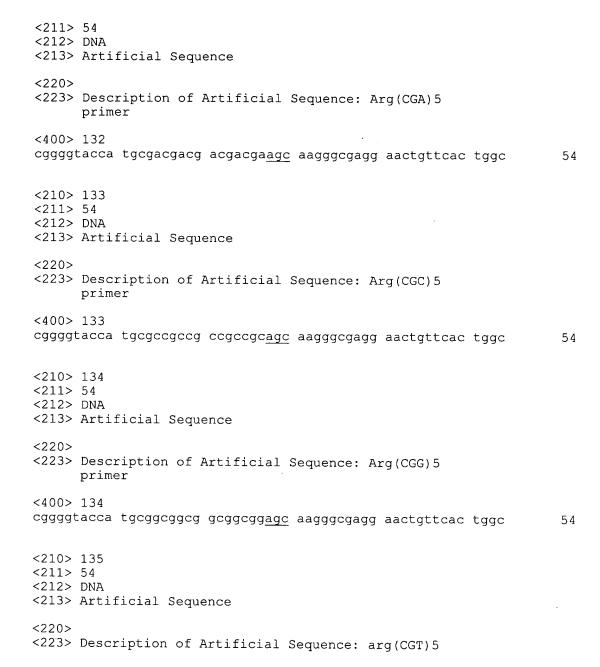
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro 180 185 190



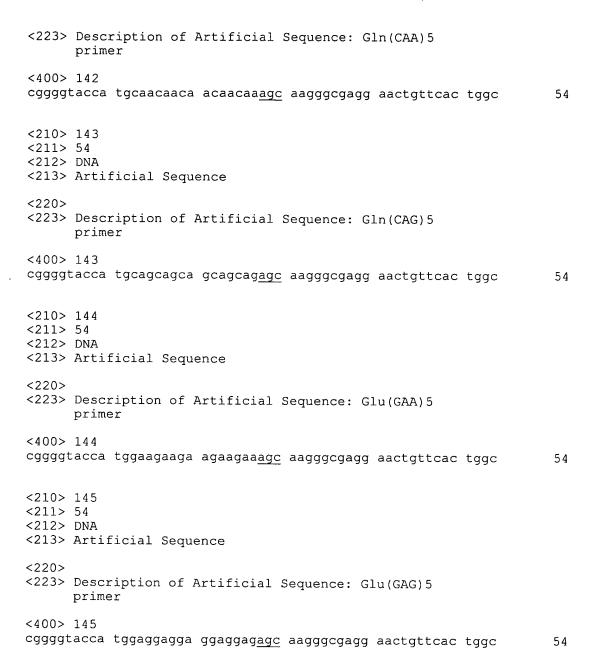






	primer	
	> 135 gtacca tgcgtcgtcg tcgtcgt <u>agc</u> aagggcgagg aactgttcac tggc	54
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	> 136 gtacca tgaacaacaa caacaac <u>agc</u> aagggcgagg aactgttcac tggc	54
<211 <212	> 137 > 54 > DNA > Artificial Sequence	
<220 <223	> Description of Artificial Sequence: Asn(AAT)5 primer	
-	> 137 gtacca tgaataataa taataat <u>agc</u> aagggcgagg aactgttcac tggc	54
<211: <212:	> 138 > 54 > DNA > Artificial Sequence	
<220: <223:	> Description of Artificial Sequence: Asp(GAC)5 primer	
	> 138 gtacca tggacgacga cgacgac <u>agc</u> aagggcgagg aactgttcac tggc	54

<210><211><211><212><213>	54	
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<210> <211> <212> <213>	54	
<220> <223>	Description of Artificial Sequence: Cys(TGC)5 primer	
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<210> <211> <212> <213>	54	
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<210><211><211><212><213>	54	
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<210> 1 <211> 5 <212> D <213> A	54	
<220> <223> D	Description of Artificial Sequence: Gly(GGA)5 primer	
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<210> 1 <211> 5 <212> D <213> A	54	
	Description of Artificial Sequence: Gly(GGC)5	
<400> 1 cggggta		54
<210> 1 <211> 5 <212> D <213> A	54	
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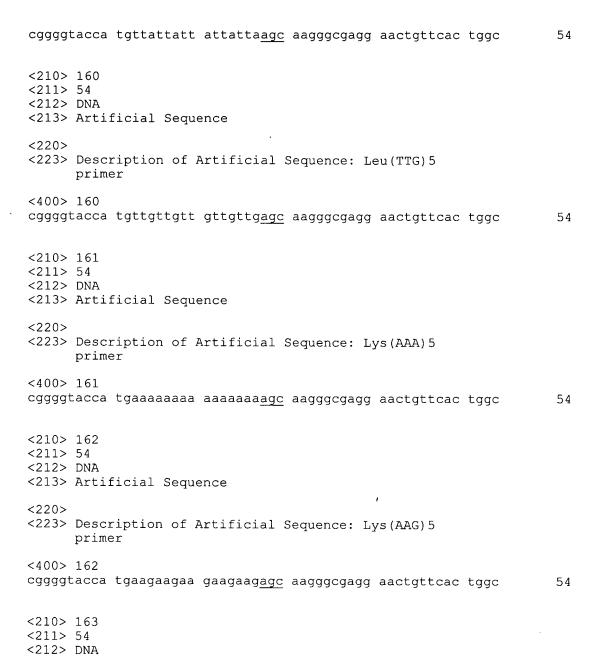
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<220> <223>	Description of Artificial Sequence: Gly(GGT)5 primer		
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<210><211><211><212><213>	54		
<220> <223>	Description of Artificial Sequence: His(CAC)5 primer		
<400> cggggt	150 acca tgcaccacca ccaccac <u>age</u> aagggcgagg aactgttcac	tggc	54
<210><211><211><212><213>	54		
<220> <223>	Description of Artificial Sequence: His(CAT)5 primer		
<400> cggggt	151 acca tgcatcatca tcatcat <u>agc</u> aagggcgagg aactgttcac	tggc	54
<210><211><211><212><213>	54		
	Description of Artificial Sequence: Ile(ATA)5 primer		
<400> cggggt	152 acca tgataataat aataata <u>agc</u> aagggcgagg aactgttcac	tggc	54



<210> 153 <211> 54 <212> DNA <213> Artificial Sequence	
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<210> 154 <211> 54 <212> DNA <213> Artificial Sequence	
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<210> 155 <211> 54 <212> DNA <213> Artificial Sequence	
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<210> 156 <211> 54 <212> DNA <213> Artificial Sequence	

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<210> <211> <212> <213>	54	
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<220> <223>	Description of Artificial Sequence: Leu(CTT)5 primer	
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<210> <211> <212> <213>	54 .	
<220> <223>	Description of Artificial Sequence: Leu(TTA)5 primer	
<400>	159	





<213>	Artificial Sequence	
<220> <223>	Description of Artificial Sequence: Phe(CTT)5 primer	
<400> cggggf	163 tacca tgcttcttct tcttctt <u>agc</u> aagggcgagg aactgttcac tggc	54
<210> <211> <212> <213>	54	٠
<220> <223>	Description of Artificial Sequence: Phe(TTC)5 primer	
<400> cggggt	164 Lacca tgttettett ettette <u>age</u> aagggegagg aactgtteae tgge	54
<210><211><211><212><213>	54	
<220> <223>	Description of Artificial Sequence: Pro(CCC)5 primer	
<400> cggggt	165 acca tgccccccc cccccc <u>agc</u> aagggcgagg aactgttcac tggc	54
<210><211><211><212><213>	54	
<220> <223>	Description of Artificial Sequence: Pro(CCG)5 primer	



<400> cggggt	166 tacca tgccgccgcc gccgccgagc aagggcgagg aactgttcac tggc	54
<210><211><211><212><213>	54	
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<210><211><211><212><213>	54	
<220> <223>	Description of Artificial Sequence: Pro(CGA)5 primer	
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<210><211><211><212><213>	54	
<220> <223>	Description of Artificial Sequence: Ser(AGC)5 primer	
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<212> <213>	DNA ' Artificial Sequence	
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<210><211><211><212><213>	54 .	
<220> <223>	Description of Artificial Sequence: Ser(TCA)5 primer	
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<210><211><211><212><213>	54.	
<220> <223>	Description of Artificial Sequence: Ser(TCC)5 primer	
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<210><211><212><212><213>	54	
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<400> cggggt	173 cacca tgtcgtcgtc gtcgtcg <u>agc</u> aagggcgagg aactgttcac tggc	54
<210><211><211><212><213>	54	
<220> <223>	Description of Artificial Sequence: Ser(TCT)5 primer	
<400> cggggt	174 cacca tgtcttcttc ttcttct <u>agc</u> aagggcgagg aactgttcac tggc	54
<210><211><211><212><213>	54	
<220> <223>	Description of Artificial Sequence: Thr(ACA)5 primer	
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<210><211><211><212><213>	54	
<220> <223>	Description of Artificial Sequence: Thr(ACC)5 primer	
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<210>	177	

54



<211><212><213>	• •
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<210> 178
<211> 54
<212> DNA
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<223> Description of Artificial Sequence: Thr(ACT)5
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<210> 179
<211> 54

<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Trp(TGG)5
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<210> 180 <211> 54 <212> DNA

<213> Artificial Sequence

<220> <223> Description of Artificial Sequence: Tyr(TAT)5





<400> 180 cggggtacca tgtattatta ttattat <u>agc</u> aagggcgagg aactgttcac tggc	54
<210> 181 <211> 54 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Val(GTA)5 primer	
<400> 181 cggggtacca tggtagtagt agtagta <u>agc</u> aagggcgagg aactgttcac tggc	54
<210> 182 <211> 54 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Val(GTC)5 primer	
<400> 182 cggggtacca tggtcgtcgt cgtcgtc <u>agc</u> aagggcgagg aactgttcac tggc	54
<210> 183 <211> 54 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Val(GTG)5 primer	
<400> 183 cggggtacca tggtggtggt ggtggtgagc aagggcgagg aactgttcac tggc	5.4





<210><211><211><212><213>	54	
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<400> cggggt	184 cacca tggttgttgt tgttgtt <u>agc</u> aagggcgagg aactgttcac tggc	54
<210> <211> <212> <213>	33	
<220> <223>	Description of Artificial Sequence: 3' oligonucleotide common primer	
<400> ccggaa	185 attc <u>t ca</u> cttgtaca ggtggtccat gcc	33